

# SEQUENCE LISTING

<110> Majumder, Kumud  
 Vernet, Corine  
 Casman, Stacie J  
 Wolenc, Adam R  
 Spaderna, Steven K  
 Padigar, Muralidhara  
 Mishnu, Vishnu S  
 Tchernev, Velizar T  
 Spytek, Kimberly A  
 Li, Li  
 Baumgartner, Jason C  
 Gusev, Vladimir

<120> Novel Proteins and Nucleic Acids Encoding Same

<130> 15966-748

<140> 09/823,172

<141> 2001-03-29

<150> 60/193,664

<151> 2000-03-31

<150> 60/194,614

<151> 2000-04-05

<150> 60/195,063

<151> 2000-04-06

<150> 60/195,066

<151> 2000-04-06

<150> 60/195,067

<151> 2000-04-06

<150> 60/195,068

<151> 2000-04-06

<150> 60/195,069

<151> 2000-04-06

<150> 60/195,070

<151> 2000-04-06

<150> 60/195,510

<151> 2000-04-06

<150> 60/219,855

<151> 2000-07-21

<150> 60/221,284

<151> 2000-07-27

<150> 60/221,325

<151> 2000-07-28

<150> 60/224,588

<151> 2000-08-11

<150> 60/239,613

<151> 2000-10-11

<150> 60/262,508

<151> 2001-01-18

<150> 60/263,604

<151> 2001-01-23

<150> 60/263,433

<151> 2001-01-23

<150> 60/265,161

<151> 2001-01-30

<160> 83

<170> PatentIn Ver. 2.1

<210> 1

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 1

```
ccgccatgta caacgggtcg tgctgccgca tcgaggggga caccatctcc caggtgatgc 60
cgccgctgct catttggtgcc tttgtgctgg gcgcactagg caatgggggt gccctgtgtg 120
gtttctgctt ccacatgaag acctgggaag ccagcactgt ttaccttttc aatttggcgc 180
tggctgattt cctccttatg atctgcctgc cttttcggac agactattac ctacagcgta 240
gacactgggc ttttggggac attcctgcc gagtggggct cttcacgttg gccatgaaca 300
gggcggggag catcgtgttc cttacggttg tggctgcgga caggtatttc aaagtgggtcc 360
acccccacca cgcggtgaac actatctcca cccgggtggc ggctggcctc gtctgcacc 420
tggtggccct ggtcatcctg ggaacagtg atcttttgc ggagaaacct ctctgcgtgc 480
aagagacggc cgtctcctgt gagagcttca tcatggagtc ggccaatggc tggcatgaca 540
tcatgttcca gctggagttc tttatgcccc tcggcatcat cttattttgc tccttcaaga 600
ttgtttggag catgaggcgg aggcagcagc tggccagaca ggctcggatg aagaaggcga 660
cccggttcac catggtggtg gcaattgtgt tcatcacatg tcatcacatg agcgtgtctg 720
ctagactcta tttcctctgg acggtgcctt cgagtgcctg cgatccctct gtccatgggg 780
cctgcacat aacctctcag ttacactaca tgaacagcat gctggatccc ctggtgtatt 840
atttttcaag cccctccttt cccaaattct acaacaagct caaaatctgc agtctgaaac 900
ccaagcagcc aggacactca aaaacacaaa ggcgggaaga gatgccaat tcgaacctcg 960
gtcgcaggag ttgcatcagt gtggcaataa gtttccaaag ccagtctgat ggccaatggg 1020
atccccacat tgttgagtgg cactgaacaa 1050
```

<210> 2

<211> 346

<212> PRT

<213> Homo sapiens

<400> 2

```
Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
1 5 10 15
```

```
Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
20 25 30
```

```
Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
35 40 45
```

```
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
50 55 60
```

```
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
65 70 75 80
```

Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala  
 85 90 95  
 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp  
 100 105 110  
 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser  
 115 120 125  
 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile  
 130 135 140  
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu  
 145 150 155 160  
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp  
 165 170 175  
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile  
 180 185 190  
 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln  
 195 200 205  
 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val  
 210 215 220  
 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg  
 225 230 235 240  
 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val  
 245 250 255  
 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met  
 260 265 270  
 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe  
 275 280 285  
 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His  
 290 295 300  
 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg  
 305 310 315 320  
 Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly  
 325 330 335  
 Gln Trp Asp Pro His Ile Val Glu Trp His  
 340 345

<210> 3  
 <211> 1050  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 tgcgcatgta caacgggtcg tgctgccgca tgcaggggga caccatctcc caggatgatgc 60  
 cgccgctgct cattgtggcc ttgtgctggt gcgcactagg caatgggggc gccctgtgtg 120  
 gtttctgctt ccacatgaag acctggaagc ccagcactgt ttaccttttc aatttggccg 180  
 tggctgattt cctccttatg atctgcctgc cttttcggac agactattac ctacagacgta 240

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| ggacactgggc | ttttgggaac  | attccctgcc  | gagtggggct | cttcacgttg  | gcatgaaca   | 300  |
| ggcgccggga  | catcgatgttc | ctacgggttg  | tggtcgggga | caggatattc  | aaagtggtcc  | 360  |
| accccccaag  | cgcggtgaac  | actatcteca  | cccggggtgc | gtcggtcatt  | gtctgaacc   | 420  |
| ttgtgggcct  | gggtcatctgt | ggagacagtg  | atcttttttg | ggagaaacct  | ctctgctgc   | 480  |
| aagagaaccc  | cgctctctgt  | ggaagcttca  | tcattggaag | ggccaatgct  | tggcatgaca  | 540  |
| tcattgttct  | gtcgtaggtc  | tttatggccc  | tcggcctcat | cttatttttg  | tccttcaaga  | 600  |
| ttgtttgag   | ctctagggcg  | aggcgacagc  | tgcccgagaa | ctgctcgatg  | aagaagaagca | 660  |
| cccgagtcct  | catgtgtgtg  | gcaattttgc  | tcatcacatg | ctcgatcgcc  | agcgctgttg  | 720  |
| cttagattct  | tttctcttgg  | acgggtgcct  | cgagtgcctg | cgatccctct  | gtccatggcg  | 780  |
| ccttgcacat  | aaacctcagc  | ttcacctaca  | tgaacagcat | gctggatccc  | ctggtgtatt  | 840  |
| atttttcaag  | cccccctctt  | cccaaaattt  | acacaagagt | caaaattctg  | agtcctgaac  | 900  |
| ccaagcagct  | aggacaacta  | aaacacacaa  | ggcccgaaag | gtgcacattc  | tgaacctcgc  | 960  |
| gtcgcgaggag | tgtcatcagt  | gtggcacaata | gtttccaaag | ccagttctgat | gggcaatggy  | 1020 |
| attccccact  | tgttgagtgt  | catctgacaa  |            |             |             | 1050 |

```
<210> 4
<211> 1104
<212> DNA
<213> Homo sapiens
```

| 400> 4      |             |             |            |             |            |      |  |
|-------------|-------------|-------------|------------|-------------|------------|------|--|
| gtgccactgtg | ggggactccc  | tgggctgctc  | tgcacccgga | cacttgtctc  | gtccccgcca | 60   |  |
| tgtacaacgg  | gtcgtgctgc  | cgcactcgagg | gggacaccat | ctcccagggtg | atgcgcgcgc | 120  |  |
| tgcctactgt  | gycctcttgg  | ctggggcgac  | tagacataag | gggtcgccctg | tgtggttttc | 180  |  |
| gtctccacat  | gaagactctg  | aagccgcgac  | ctgtttaact | tttccaattg  | gcgctggctg | 240  |  |
| atttctectc  | tatgatctgc  | ctgccttttc  | ggacagacta | tttacctaga  | cgtagacact | 300  |  |
| gggctcttgg  | ggacatctcc  | tggcagatgg  | ggctctctac | gttgggcact  | aacaggcgcg | 360  |  |
| ggagcatctg  | gttctctaac  | gtgtggctgt  | cgggcaggta | tttccaaagt  | gtccaccctc | 420  |  |
| acacacggcg  | gaacactatc  | tcacacgggg  | tggcggctgg | cattcgctgc  | acctctggg  | 480  |  |
| ccctggctcat | ctctgggaac  | gtgtatcttt  | tgtcggagaa | ccatctctgc  | gtcgcaagaa | 540  |  |
| cggcgctctc  | ctgtgagagc  | tgcatactgc  | agtcggccaa | tggctggcat  | gacatcatgt | 600  |  |
| tcacgtctgc  | gtttctttatg | cccctcgcca  | tcatcttatt | ttgctctctc  | aagatctgtt | 660  |  |
| ggagcctgag  | goggaggcag  | cagctggcca  | gacaggctcg | gatgaagaag  | gcgacacggg | 720  |  |
| tcactcatggt | gggtggcaatt | gtgttctaca  | catgctacct | gccacgagtg  | ttctgtcaga | 780  |  |
| tctatttctt  | ctggagcgggt | ctccagatgt  | cgctcgatcc | ctgtgtccat  | ggggccctcg | 840  |  |
| acataacctc  | cagctctaac  | tacatgaaca  | cgatgctgta | tcctcctgtg  | tattattttt | 900  |  |
| caagcccttc  | cttttccaaa  | tcttacaaca  | agctacaaat | ctatgctgtc  | aaaccacaag | 960  |  |
| acgcaggaaa  | ctcaaaaaca  | caaaggccgg  | aagagatgcc | atcttcgtae  | ctcggctgca | 1020 |  |
| ggagttgcat  | cagtgctgga  | aatagtttcc  | aaagccagtc | tgatgggcaa  | tgggatcccc | 1080 |  |
| acattgttga  | gtgcgactga  | acaa        |            |             |            | 1140 |  |

```
<210> 5
<211> 346
<212> PRT
<213> Homo sapiens
```

Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala  
 85 90 95  
 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Gly  
 100 105 110  
 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser  
 115 120 125  
 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile  
 130 135 140  
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu  
 145 150 155 160  
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp  
 165 170 175  
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile  
 180 185 190  
 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Gln Gln  
 195 200 205  
 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val  
 210 215 220  
 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg  
 225 230 235 240  
 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val  
 245 250 255  
 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met  
 260 265 270  
 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe  
 275 280 285  
 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His  
 290 295 300  
 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg  
 305 310 315 320  
 Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly  
 325 330 335  
 Gln Trp Asp Pro His Ile Val Glu Trp His  
 340 345

<210> 6  
 <211> 1149  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 atggccgatg cagccacgat agccaccatg aataaggcag caggcgggga caagctagca 60  
 gaactcttca gtctggtccc ggaccttctg gagcggccca acacagtggt taacgcgctcg 120  
 ctgcagcttc cggacttggt gtgggagctg gggctggagt tgccggacgg cgcgccgcca 180  
 ggacatcccc cgggcagcgg cggggcagag agcgcggaca cagagggccc ggtgcggatt 240

```

ctctacagcg tgggtgactg ggtggtgtgc gccctggggt tggcgggcaa cctgctgttt 300
ctctacctga tgaagagcat gcagggtctg cgaagtcct ctatcaacct cttcgtcaacc 360
aacctggcgc tgacggactt tcagttttgt ctcacctgc cctctctggc ggtggagaac 420
gctctgact tcaaatggcc cttcggcaag gccatgtgta agatcgtgtc catggtgacg 480
tccatgaaca tgtaaccgag cgtgttctt ctaactgcc tgagtgtgac gcgctaccat 540
tcggtggcct cggtctctga gagccaccgg acccgaggac acggccgggg cgactgtgtc 600
ggccggagcc tgggggacag ctgctgtctt tcggccaagg cgctgtgtgt gtggtcttgg 660
gctttggcgc cgtgggctc gctgcccagt gccattttct ccaccaagg caaggtgatg 720
ggcgaggagc tgtgcaactg tgcgtttccc ggacaagtgt ctggggccgc acaggcagtt 780
ctggctgggc ctctaccact cgcagaagaa gctgctgggg taccgctta cttagcatat 840
atttttattc caaacaatt ctttagatca ctacctctt cttacgacct cttgtatttt 900
ccgccctctt cttacccttc cgttatccgc aacatttctt cttaccgcc acaacagat 960
aaaccgcgta ggacctggtg tccaccccca tggactggac ccgccagtc agaccagatt 1020
gaaaatacgt atagatttgc tacctgctat gtacatcaat atgaatttct ggcatttaaa 1080
tcaaacagat ttccaggaac tagcctgggg actcagacac catttaaac ttgggaaagc 1140
atgttttga

```

```

<210> 7
<211> 382
<212> PRT
<213> Homo sapiens

```

```

<400> 7
Met Ala Asp Ala Ala Thr Ile Ala Thr Met Asn Lys Ala Ala Gly Gly
1 5 10 15
Asp Lys Leu Ala Glu Leu Phe Ser Leu Val Pro Asp Leu Leu Glu Ala
20 25 30
Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu Trp Trp
35 40 45
Glu Leu Gly Leu Glu Leu Pro Asp Gly Ala Pro Pro Gly His Pro Pro
50 55 60
Gly Ser Gly Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val Arg Ile
65 70 75 80
Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu Ala Gly
85 90 95
Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp Arg Lys
100 105 110
Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp Phe Gln
115 120 125
Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu Asp Phe
130 135 140
Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met Val Thr
145 150 155 160
Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met Ser Val
165 170 175
Thr Arg Tyr His Ser Val Ala Ser Ala Leu Lys Ser His Arg Thr Arg
180 185 190
Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp Ser Cys
195 200 205

```

Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu Ala Ala  
 210 215 220  
 Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys Val Met  
 225 230 235 240  
 Gly Glu Glu Leu Cys Thr Gly Ala Phe Pro Gly Gln Val Ala Gly Pro  
 245 250 255  
 Arg Gln Ala Val Leu Ala Gly Pro Leu Pro Leu Ala Glu Glu Ala Ala  
 260 265 270  
 Gly Val Pro Ala Tyr Leu Ala Tyr Ile Phe Ile Pro Lys Gln Phe Phe  
 275 280 285  
 Arg Ser Leu Pro Leu Ser Tyr Asp Leu Leu Tyr Phe Pro Pro Leu Ser  
 290 295 300  
 Tyr Pro Ser Val Ile Arg Asn Ile Ser Ser Leu Pro Pro Gln His Asp  
 305 310 315 320  
 Lys Pro Arg Arg Thr Trp Cys Pro Pro Pro Trp Thr Gly Pro Ala Ser  
 325 330 335  
 Pro Asp Gln Ile Glu Asn Thr Tyr Arg Phe Ala Thr Cys Tyr Val His  
 340 345 350  
 His Tyr Glu Phe Leu Ala Phe Lys Ser Asn Arg Phe Ser Gly Thr Ser  
 355 360 365  
 Leu Gly Thr Gln Thr Pro Phe Lys Pro Trp Glu Ser Met Phe  
 370 375 380

<210> 8  
 <211> 970  
 <212> DNA  
 <213> Homo sapiens

<400> 8  
 aaaaagtctc cagaagaacg gcctcaatga ataccactct atttcatect tactctttcc 60  
 ttcttctggg aattcctggg ctggaaagta tgcactctct ggttggtttt cctttctttg 120  
 ctgtgttctc gacagctgtc ctgggaata tcaccatctt ttttgtgatt cagactgaca 180  
 gtagtctcca tcattccatg ttctacttcc tggccattct gtcattctatt gaccctgggc 240  
 tgtctacatc caccatccct aaaatgcttg gcacctcttg gtttaccctg agagaaatct 300  
 cctttgaagg atgccttacc cagatgttct tcattccact gtgcactggc atggaatcag 360  
 ctgtgcttgt ggccatggcc tatgattgct atgtggccat ctgtgacctt ctttgtctaca 420  
 cgttgtgctt gacaaacaag gtggtgtcag ttatggcact ggccattctt ctgagacctt 480  
 tagtctttgt catacccttt gtctatttta tcttaaggct tccattttgt ggacacccaa 540  
 ttattctcca tacttatggg gaggacatgg gcattgcccg cctgtcttgt gccagcatca 600  
 gggttaacat catctatggc ttatgtgccca tctctatctt ggtctttgac atcatagcaa 660  
 ttgtcatttc ctatgtacag atcctttgtg ctgtatttct actctcttca catgatgcac 720  
 gactcaaggc attcagcacc tgtggctctc atgtgtgtgt catgttgact tcttatatgc 780  
 ctgcattttt ctcatctcat acccataggt ttggtcgga tatactcac ttattccaca 840  
 ttctcttggc taattttctat gtatgcattc cacctgctct caactctgta atttatgggt 900  
 tcagaaccaa acagattaga gcacaagtgc tgaaaaatgt tttcaataaa taaaacatag 960  
 ctcatattata

<210> 9  
 <211> 308  
 <212> PRT  
 <213> Homo sapiens

<400> 9

Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile  
1 5 10 15

Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala  
20 25 30

Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile  
35 40 45

Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile  
50 55 60

Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met  
65 70 75 80

Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys  
85 90 95

Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala  
100 105 110

Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro  
115 120 125

Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala  
130 135 140

Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu  
145 150 155 160

Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr  
165 170 175

Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg  
180 185 190

Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp  
195 200 205

Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe  
210 215 220

Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly  
225 230 235 240

Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser  
245 250 255

Phe Met Thr His Arg Phe Gly Arg Asn Ile Pro His Phe Ile His Ile  
260 265 270

Leu Leu Ala Asn Phe Tyr Val Val Ile Pro Pro Ala Leu Asn Ser Val  
275 280 285

Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Ala Gln Val Leu Lys Met  
290 295 300

Phe Phe Asn Lys  
305



<210> 10  
 <211> 994  
 <212> DNA  
 <213> Homo sapiens

<400> 10  
 tgctgaatta ctcaaagtca ctatgggaga ctggaataac agtgaatgctg tggagcccat 60  
 atttatcctg aggggttttc ctggactgga gtaatgttcat tcttggctct ccatcctctt 120  
 ctgtctctga tatcttgtag catttatggg taatgttacc atcctgtctg tcatttggat 180  
 agaatcctct ctccatcagc ccatgtatta ctttatttcc atcttagcag tgaatgacct 240  
 ggggagtgtcc ctgtctacac ttcccaccat gcttgcgtgt ttatgggttg atgtccaga 300  
 gatccaggca agtgccttgc atgctcagct gttcttcac cacaattca cattcctgga 360  
 gtctctcagtg ttgctggcca tggcctttga cggttttgtt gctatctgcc atccactgca 420  
 ctaccccacc atcctcacca acagtgtaat tggcaaaatt ggtttggcct gtttgctacg 480  
 aagcttgagg gttgtacttc ccacaccttt gctactgaga cactataact actgccatgg 540  
 caatgccctc tctcacgcct tctgtttgca ccaggatgtt ctaagattat cctgtacaga 600  
 tggcagggacc aacagtattt atgggctttg ttagtgcatt gccacactag gctgggattc 660  
 aatcttcata ctctcttctt atgttctgat tcttaatact gtgctggata ttgcatctcg 720  
 tgaagagcag ctaaaaggcac tcaacacatg tgtatcccat atctgtgtgg tgtctatctt 780  
 ctttgtgcca gttattgggg tgtcaatggt ccatcgcttt gggaagcacc tgtctcccat 840  
 agtccacatc ctcatggcag acatctacct tcttcttccc ccagtcctta accctattgt 900  
 ctatagtgtc agaacaaagc agattcgtct aggaattctc cacaagtgtg tcctaaggag 960  
 gagggttttaa gtaacctctg tctccaact tttc 994

<210> 11  
 <211> 315  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
 Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu  
 1 5 10 15  
 Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu  
 20 25 30  
 Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu  
 35 40 45  
 Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe  
 50 55 60  
 Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu  
 65 70 75 80  
 Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala  
 85 90 95  
 Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu  
 100 105 110  
 Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly  
 130 135 140  
 Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro  
 145 150 155 160  
 Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu  
 165 170 175

Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr  
180 185 190

Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr  
195 200 205

Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu  
210 215 220

Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu  
225 230 235 240

Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro  
245 250 255

Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro  
260 265 270

Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val  
275 280 285

Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Arg Leu Gly  
290 295 300

Ile Leu His Lys Phe Val Leu Arg Arg Arg Phe  
305 310 315

<210> 12  
<211> 994  
<212> DNA  
<213> Homo sapiens

<400> 12  
tgc tgaatta ctcaaagtc ctatgggaga ctggaataac agtgatgctg tggagcccat 60  
attatcctg aggggttttc ctggactgga gtatgttcac tcttggtctt ccactccttt 120  
ctgtcttgca tatttggttag catttatggg taatgtttacc atcctgtctg tcatttggat 180  
agaatectet ccccatcagc ccatgtatta ctttatttcc atcttggcag tgaatgaact 240  
ggggatgtcc ctgtctacac ttcccacccat gcttgtctgt ttatggttg atgctccaga 300  
gatccaaggca agtgcttgct atgctcagct gtctctcatc cacacattca cattctgga 360  
gtctcagtg ttgtggcca tggcctttga cgttttgtt gctatctgcc atccactgca 420  
ctacccacc atctccacca acagtgtaat tggcaaaatt ggttggcct gtttgcacg 480  
aagcttggga gttgtacttc ccacaccttt gctactgaga cactatcact actgccatgg 540  
caatgccctc tctcagcct tctgtttgca ccaggatgtt ctaagattat cctgtacaga 600  
tgccaggacc aacagtattt atgggctttg tgtagtcatt gccacactag gtgtggattc 660  
aatcttcata ctctctttct atgtctgtat tcttaatact gtgctggata ttgcatctcg 720  
tgaagagcag cttaaaggcac tcaacacatg tgtatcccat atctgtgtgg tgcttatctt 780  
ctttgtgcca gttattgggg tgtcaatggt ccactgcttt gggaagcacc tgtctcccat 840  
agtcacatc ctcatggcag acatgtacct tctctctccc ccagtccta accctattgt 900  
ctatagtgtc agaacaagc agattcgtct aggaattctc cacaagtttg tcctaaggag 960  
gagggttttaa gtaactctg tctccaact ttcc 994

<210> 13  
<211> 315  
<212> PRT  
<213> Homo sapiens

<400> 13  
Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu  
1 5 10 15

Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu  
 20 25 30  
 Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu  
 35 40 45  
 Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe  
 50 55 60  
 Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu  
 65 70 75 80  
 Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala  
 85 90 95  
 Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu  
 100 105 110  
 Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile  
 115 120 125  
 Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly  
 130 135 140  
 Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro  
 145 150 155 160  
 Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu  
 165 170 175  
 Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr  
 180 185 190  
 Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr  
 195 200 205  
 Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu  
 210 215 220  
 Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu  
 225 230 235 240  
 Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro  
 245 250 255  
 Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro  
 260 265 270  
 Ile Val His Ile Leu Met Ala Asp Met Tyr Leu Leu Leu Pro Pro Val  
 275 280 285  
 Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Arg Leu Gly  
 290 295 300  
 Ile Leu His Lys Phe Val Leu Arg Arg Arg Phe  
 305 310 315

<210> 14  
 <211> 994  
 <212> DNA  
 <213> Homo sapiens

<400> 14  
 tgctgaattc ctcaaagtc ctatgggaga ctggaataac agtgatgctg tggagcccat 60  
 atttatctcg aggggttttc ctggactgga gtatgttcac tcttggtctt ccacacctct 120  
 ctgtcttgca tatttggtag catttatggg taatgttacc atcctgtctg tcatttggat 180  
 agaatcctct ctccatcagc ccattgtatt ctttatttcc atcttggcag tgaatgacct 240  
 ggggagtgtc ctgtctacac tccccaccat gcttgctgtg ttatgggttg atgtccaga 300  
 gatccaggca agtgctgtct atgtctcagct gttcttctac cacacattca catttctgga 360  
 gtctcagctg ttgctggcca tggcctttga cggttttgtt gctatctgcc atccactgca 420  
 ctacccccacc atctccacca acagtgtaat tggcaaaatt gggttggcct gtttgcacg 480  
 aagcttgagg gtgtacttc ccacaccttt gctactgaga cactcact actgcatctg 540  
 caatgccttc tctcagcct tctgtttgca ccaggatgtt ctaagattat cctgtacaga 600  
 tggccaggacc aacagatttt atgggctttg tgtagtcat gccacactag gtgtgattc 660  
 aatcttcata ctctctttt atgttctgat tcttaatact gtgctggata tgcactctg 720  
 tgaagagcag ctaaaagcac tcaacacatg tgtatcccat atctgtgtgg tgcattatct 780  
 ctttctgcca gtattgggg tgtcaatggg ccactgcttt gggaagcac tgcctcccat 840  
 agtccacatc ctaactggag acatctacct tcttcttccc ccagtcctta accctattgt 900  
 ctatagtgtc agaacaagc agattcgtct aggaattctc cacaagtttg tctcaaggag 960  
 gaggttttaa gtaacctctg tctccaact tttc 994

<210> 15  
 <211> 985  
 <212> DNA  
 <213> Homo sapiens

<400> 15  
 gttctcctac actgtgattt ggaaaaatgt tttatcacaa caagagcata tttcaccag 60  
 tcacattttt cctcattgga atcccaggct tgggaagact ccacatgtgg atctccggc 120  
 cttctcgtct tgtttaccct gtggccttgc tgggcaatgc caccattctg ctatgcata 180  
 aggtagaaca gactctccgg gagcccatgt tctacttctt ggccattctt tccaacttg 240  
 atttgccctt tttgcaacc tctgtgcctc gcactgtggg tatctctggt ttgatgctc 300  
 acgagattaa ctatggagct tgtgtggccc agatgtttct gctacatgcc ttaactgcca 360  
 tggaggtgta ggtcttactg gctatggcct ttgaccgtta tgtggccatc tgtgtccac 420  
 tacattacgc aacctcttgc acatccctag tgttgggtgg cattagcatg tgcattgtaa 480  
 ttctgtccgt ttactttaca cttcccatgg tctatcttat caccgoccta cctctttgtc 540  
 aggtccacat aatagcccat tctactgtg agcacatggg cattgcaaaa ttgtcctgtg 600  
 gaacaccatg tatcaatggt atctatgggc tttttgtagt tttcttcttt tgtctgaacc 660  
 tgggtgtctc tggcactctg tatgtttaca tcttccgtgc tgtcttccgc ctcccatcac 720  
 atgatgtcca gctaaaagcc ctaagcacgt gtggcgctca tgttggagtc atctgtgttt 780  
 tctatctccc ttcagttctc tctttcttta ctcactgatt tggacaccaa ataccaggtt 840  
 acattcacat tctgtttgcc aatctctatt tgattatccc accctctctc aaccccatca 900  
 tttatggggg gaggacaaa cagattcgag agcgagtgct ctatgttttt actaaaaaat 960  
 aagactctta ccatgttatt ttact 985

<210> 16  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Phe Tyr His Asn Lys Ser Ile Phe His Pro Val Thr Phe Phe Leu  
 1 5 10 15  
 Ile Gly Ile Pro Gly Leu Glu Asp Phe His Met Trp Ile Ser Gly Pro  
 20 25 30  
 Phe Cys Ser Val Tyr Leu Val Ala Leu Leu Gly Asn Ala Thr Ile Leu  
 35 40 45  
 Leu Val Ile Lys Val Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr Phe  
 50 55 60

Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Ala Thr Ser Val  
 65 70 75 80  
 Pro Arg Met Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn Tyr  
 85 90 95  
 Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly Met  
 100 105 110  
 Glu Ala Glu Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Ala Pro Leu His Tyr Ala Thr Ile Leu Thr Ser Leu Val Leu Val  
 130 135 140  
 Gly Ile Ser Met Cys Ile Val Ile Arg Pro Val Leu Leu Thr Leu Pro  
 145 150 155 160  
 Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile  
 165 170 175  
 Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly  
 180 185 190  
 Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe  
 195 200 205  
 Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg  
 210 215 220  
 Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser  
 225 230 235 240  
 Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser  
 245 250 255  
 Val Phe Ser Phe Leu Thr His Arg Phe Gly His Gln Ile Pro Gly Tyr  
 260 265 270  
 Ile His Ile Leu Val Ala Asn Leu Tyr Leu Ile Ile Pro Pro Ser Leu  
 275 280 285  
 Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val  
 290 295 300  
 Leu Tyr Val Phe Thr Lys Lys  
 305 310

<210> 17  
 <211> 947  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
 tgaaaaatgt tttatcacaa caagagcata tttcaccag tcacattttt cctcattgga 60  
 atcccagggt tgggaagactt ccacatgtgg atctcggggc ctttctgctc tgtttacctt 120  
 gtggctttgc tgggcaatgc caccattctg ctagtcatca aggtagaaca gacttcagg 180  
 gagcccatgt tctacttctt ggccattctt tccactattg atttggccct ttctacaacc 240  
 tctgtgcttc gcatgctggg tatcttctgg ttgatgctc acgagattaa ctatggagct 300  
 tgtgtggccc agatgtttct gatccatgcc ttcactggca tggaggctga ggtcttactg 360  
 gctatggcctt ttgaccgtta tgtggcgcgc tgtgtccac tacattacgc aaccatcttg 420  
 acatcccaag tgttggtggg cattagcatg tgcattgtaa tccgtcccgct tttacttaca 480

cttcccatgg tctatcttat ctaccgccta ccccttttgc aggcacacat aatagcccat 540  
 tctactgtg agcacatggg cattgcacaaa ttgtcctgtg gaaacattcg tatcaatggg 600  
 atctatgggc tttttgtagt ttctctcttt gtctcgaacc tgggtgctcat tggcatctcg 660  
 tatgtttaca ttctccgtgc tgtcttcgcg ctcccatcac atgatgctca gctaaaagcg 720  
 ctaagcacgt gtggcgctca tgttgagtc atctgtgttt tctatatccc ttcagttctc 780  
 tctttcetta ctcatcgatt tggacaccaa ataccaggtt acattcatt tctgttgccc 840  
 aatctctatt tgattatccc accctctctc aaccccatca tttatggggg gaggacacaa 900  
 cagattcgag aacgagtgcct ctatgttttt actaaaaaat aagacta 947

<210> 18  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Met Phe Tyr His Asn Lys Ser Ile Phe His Pro Val Thr Phe Phe Leu  
 1 5 10 15  
 Ile Gly Ile Pro Gly Leu Glu Asp Phe His Met Trp Ile Ser Gly Pro  
 20 25 30  
 Phe Cys Ser Val Tyr Leu Val Ala Leu Leu Gly Asn Ala Thr Ile Leu  
 35 40 45  
 Leu Val Ile Lys Val Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr Phe  
 50 55 60  
 Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Thr Thr Ser Val  
 65 70 75 80  
 Pro Arg Met Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn Tyr  
 85 90 95  
 Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly Met  
 100 105 110  
 Glu Ala Glu Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Val  
 115 120 125  
 Cys Ala Pro Leu His Tyr Ala Thr Ile Leu Thr Ser Gln Val Leu Val  
 130 135 140  
 Gly Ile Ser Met Cys Ile Val Ile Arg Pro Val Leu Leu Thr Leu Pro  
 145 150 155 160  
 Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile  
 165 170 175  
 Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly  
 180 185 190  
 Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe  
 195 200 205  
 Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg  
 210 215 220  
 Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser  
 225 230 235 240  
 Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser  
 245 250 255

Val Phe Ser Phe Leu Thr His Arg Phe Gly His Gln Ile Pro Gly Tyr  
260 265 270

Ile His Ile Leu Val Ala Asn Leu Tyr Leu Ile Ile Pro Pro Ser Leu  
275 280 285

Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val  
290 295 300

Leu Tyr Val Phe Thr Lys Lys  
305 310

<210> 19  
<211> 945  
<212> DNA  
<213> Homo sapiens

<400> 19  
gaaaaatggtt ttatcacaca aagagcatat ttcacccagt cacatttttc ctcattggaa 60  
tcccagggtct ggaagacttc cacatgtgga tctccgggcc tttctgctct gtttaccttg 120  
cggetttgct gggcaatgcc accattctgc tagtcatcaa ggtagaacag actctccggg 180  
agcccatggt ctacttctct gccattcttt ccactattga tttggccctt tctacaacct 240  
ctgtgacctg catgctgggt atcttctggt ttgatgctca cagagattaac tatggagctt 300  
gtgtggccca gatgtttctg atccatgctt tcactggcat ggaggctgag gtcttactgg 360  
ctatggcttt tgaccgttat gtggccgtct gtgctccact acattacgca accatcttga 420  
catcccaagt gttggtgggc attagcatgt gcattgtaat tegtcccggt ttacttacac 480  
ttcccatggt ctatcttacc taccgcctac ccttttgta ggtccacata atagccatt 540  
cctactgtga gcacatgggc attgcaaaat tgtcctgtgg aaacattcgt atcaatggta 600  
tctatgggct tttttagtatt tctttctttg ttctgaacct ggtgctcatt ggcatctcgt 660  
atgtttacat tctcgtgct gtcttccgcc tcccatcaca tgatgctcag ctaaaagccc 720  
taagcacgtg tggcgctcat gttggagtc tctgtgtttt ctatatccct tcagctctct 780  
ctttcttacc tcatcgattt ggacaccaaa taccaggtta cattcacatt ctgtgtgcca 840  
atctctattt gattatccca cctctctca accccatcat ttatgggggtg aggaccaaac 900  
agattcgaga acgagtgctc tatgttttta ctaaaaaata agact 945

<210> 20  
<211> 311  
<212> PRT  
<213> Homo sapiens

<400> 20  
Met Phe Tyr His Asn Lys Ser Ile Phe His Pro Val Thr Phe Phe Leu  
1 5 10 15  
Ile Gly Ile Pro Gly Leu Glu Asp Phe His Met Trp Ile Ser Gly Pro  
20 25 30  
Phe Cys Ser Val Tyr Leu Ala Ala Leu Leu Gly Asn Ala Thr Ile Leu  
35 40 45  
Leu Val Ile Lys Val Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr Phe  
50 55 60  
Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Thr Thr Ser Val  
65 70 75 80  
Pro Arg Met Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn Tyr  
85 90 95  
Gly Ala Cys Val Ala Gln Met Phe Leu Ile Phe Thr Gly Met  
15





agaaccaagc agatctataa atgtgtaaag aaaatattat tgcaggaaca aggaatggaa 960  
 aaggaagagt acctaataca tacgaggttc tgaatgcaat tttatgaaat tt 1012

<210> 22  
 <211> 325  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Met Phe Leu Pro Asn Asp Thr Gln Phe His Pro Ser Ser Phe Leu Leu  
 1 5 10 15  
 Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro  
 20 25 30  
 Phe Cys Ala Val Tyr Met Ile Ala Leu Ile Gly Asn Phe Thr Ile Leu  
 35 40 45  
 Leu Val Ile Lys Thr Asp Ser Ser Leu His Gln Pro Met Phe Tyr Phe  
 50 55 60  
 Leu Ala Met Leu Ala Thr Thr Asp Val Gly Leu Ser Thr Ala Thr Ile  
 65 70 75 80  
 Pro Lys Met Leu Gly Ile Phe Trp Ile Asn Leu Arg Gly Ile Ile Phe  
 85 90 95  
 Glu Ala Cys Leu Thr Gln Met Phe Phe Ile His Asn Phe Thr Leu Met  
 100 105 110  
 Glu Ser Ala Val Leu Val Ala Met Ala Tyr Asp Ser Tyr Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Gln Tyr Ser Ala Ile Leu Thr Asn Lys Val Val Ser  
 130 135 140  
 Val Ile Gly Leu Gly Val Phe Val Arg Ala Leu Ile Phe Val Ile Pro  
 145 150 155 160  
 Ser Ile Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Asn His Val Ile  
 165 170 175  
 Pro His Thr Tyr Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ala  
 180 185 190  
 Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Cys Ala Ile Cys Asn Leu  
 195 200 205  
 Val Phe Asp Ile Thr Val Ile Ala Leu Ser Tyr Val His Ile Leu Cys  
 210 215 220  
 Ala Val Phe Arg Leu Pro Thr His Glu Pro Arg Leu Lys Ser Leu Ser  
 225 230 235 240  
 Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala  
 245 250 255  
 Leu Phe Ser Phe Met Thr His Cys Phe Gly Arg Asn Val Pro Arg Tyr  
 260 265 270  
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu  
 275 280 285

Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Lys Cys Val  
290 295 300

Lys Lys Ile Leu Leu Gln Glu Gln Gly Met Glu Lys Glu Glu Tyr Leu  
305 310 315 320

Ile His Thr Arg Phe  
325

<210> 23  
<211> 1012  
<212> DNA  
<213> Homo sapiens

<400> 23  
gcattcacaa gcaggatggt ccttccaat gacaccagtt ttcacccctc ctccttctctg 60  
ttgctgggga tcccaggact agaaacactt cacatctgga tcggctttcc cttctgtgct 120  
gtgtacatga tcgcactcat agggaaacttc actattctac ttgtgatcaa gactgacagc 180  
agcctacacc agcccatggt ctaacttcctg gccatgttgg ccaccactga tgtgggtctc 240  
tcaacagcta ccatccctaa gatgcttgga atctcttgga tcaacctcag agggatcatc 300  
tttgaagcct gcctcaccca gatgtttttt atccacaact tcacacttat ggagtcagca 360  
gtccttgtgg caatgggtta tgacagctat gtggccactc gcaatccaat ccaatatagc 420  
gccatcctca ccaacaaggt tgttctgtg attgggtctg gtgtgtttgt gagggcttta 480  
atcttctgca ttcctctcat acttcttata ttggggttgc cctctctgtg gaatcatgta 540  
attccccaca cctactgtga gcacatgggt cttgctcatc tatcttgtgc cagcatcaaa 600  
atcaatatta tttatgggtt atgtgccatt tgtaactcag tgtttgacat cacagtcatt 660  
gcctctcttt atgtgcatat tctttgtgct gttttccgtc ttcctactca tgaagcccga 720  
ctcaagtcct tcagacacatg tgggtcacat gtgtgtgtaa tccttgccct ctatacacca 780  
gcctcttttt cctttatgac tcatcgcttt ggccgaaatg tgccccgcta tatccatata 840  
ctctagcca atctctatgt tgtggtgcca ccaatgctca atcctgtcat atatggagtc 900  
agaaccaagc agatctataa atgtgtgaag aaaatattat tgcaggaaca aggaatggaa 960  
aggaagagt acctaataca tacgaggttc tgaatgcaat tttatgaaat tt 1012

<210> 24  
<211> 325  
<212> PRT  
<213> Homo sapiens

<400> 24  
Met Phe Leu Pro Asn Asp Thr Gln Phe His Pro Ser Ser Phe Leu Leu  
1 5 10 15  
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro  
20 25 30  
Phe Cys Ala Val Tyr Met Ile Ala Leu Ile Gly Asn Phe Thr Ile Leu  
35 40 45  
Leu Val Ile Lys Thr Asp Ser Ser Leu His Gln Pro Met Phe Tyr Phe  
50 55 60  
Leu Ala Met Leu Ala Thr Thr Asp Val Gly Leu Ser Thr Ala Thr Ile  
65 70 75 80  
Pro Lys Met Leu Gly Ile Phe Trp Ile Asn Leu Arg Gly Ile Ile Phe  
85 90 95  
Glu Ala Cys Leu Thr Gln Met Phe Phe Ile His Asn Phe Thr Leu Met  
100 105 110

Glu Ser Ala Val Leu Val Ala Met Ala Tyr Asp Ser Tyr Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Gln Tyr Ser Ala Ile Leu Thr Asn Lys Val Val Ser  
 130 135 140  
 Val Ile Gly Leu Gly Val Phe Val Arg Ala Leu Ile Phe Val Ile Pro  
 145 150 155 160  
 Ser Ile Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Asn His Val Ile  
 165 170 175  
 Pro His Thr Tyr Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ala  
 180 185 190  
 Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Cys Ala Ile Cys Asn Leu  
 195 200 205  
 Val Phe Asp Ile Thr Val Ile Ala Leu Ser Tyr Val His Ile Leu Cys  
 210 215 220  
 Ala Val Phe Arg Leu Pro Thr His Glu Ala Arg Leu Lys Ser Leu Ser  
 225 230 235 240  
 Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala  
 245 250 255  
 Leu Phe Ser Phe Met Thr His Arg Phe Gly Arg Asn Val Pro Arg Tyr  
 260 265 270  
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu  
 275 280 285  
 Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Lys Cys Val  
 290 295 300  
 Lys Lys Ile Leu Leu Gln Glu Gln Gly Met Glu Lys Glu Glu Tyr Leu  
 305 310 315 320  
 Ile His Thr Arg Phe  
 325

<210> 25  
 <211> 968  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
 tcttcacgat ggtggatccc aatggcaatg aatccagatgc tacatacttc atcctaataag 60  
 gccctccctgg tttagaagag gctcagttct ggttggcctt cccattgtgc tcctctatacc 120  
 ttattgtctgt gctaggtaac ttgacaatca tctacattgt gcggactgag cacagcctgc 180  
 atgagcccat gtatatattt ctttgcacgc tttcaggcat tgacatccctc atctccacct 240  
 catccatgcc caaaatgctg gccatcttct ggttcaattc cactaccatc cagtttgatg 300  
 ottgtctgct acagatgttt gccatccact ccttatctgg cctggaatcc acagtgtgc 360  
 tggccatggc ttttgaccgc tatgtggcca tctgtcaccc actgcccact gccacagtac 420  
 ttacgttgcc tcgtgtcacc aaaattgggt tggctgctgt ggtgcggggg gctgcaactga 480  
 tggcacccct tcctgtcttc atcaagcagc tgcccttctg ccgctccaat atcctttccc 540  
 attcctactg cctacaccaa gatgtcatga agctggcctg tgatgatata cgggtcaatg 600  
 tcgtctatgg ccttatcgtc atcatctccg ccaatggcct ggactcactt ctcactctct 660  
 tctcatatct gcttattctt aagactgtgt tgggcttgac acgtgaagcc caggccaagg 720  
 catttggaac ttgcgtctct catgtgtgtg ctgtgttcat attctatgta ctttctattg 780  
 gattgtccat ggtgcacgc tttagcaagc ggcgtgactc tccgctgccc gtcactttgg 840

ccaatatcta tctgctggtt cctcctgtgc tcaacccaat tgtctatgga gtgaagacaa 900  
 aggagattgc acagcgcac cttcgacttt tccatgtggc cacacacgct tcagagccct 960  
 aggtgtca 968

<210> 26  
 <211> 318  
 <212> PRT  
 <213> Homo sapiens

<400> 26  
 Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile  
 1 5 10 15  
 Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe  
 20 25 30  
 Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile  
 35 40 45  
 Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile  
 50 55 60  
 Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser  
 65 70 75 80  
 Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln  
 85 90 95  
 Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly  
 100 105 110  
 Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val  
 130 135 140  
 Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala  
 145 150 155 160  
 Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile  
 165 170 175  
 Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys  
 180 185 190  
 Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser  
 195 200 205  
 Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile  
 210 215 220  
 Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe  
 225 230 235 240  
 Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro  
 245 250 255  
 Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser  
 260 265 270  
 Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val

Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg  
290 295 300

Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro  
305 310 315

<210> 27  
<211> 969  
<212> DNA  
<213> Homo sapiens

<400> 27  
ttcttcatga tgggtgatcc caatggcaat gaatccagtg ctacatactt catcctaata 60  
ggcctccctg gtttagaaga ggctcagttc tgggtggcct tccattgtg ctcctctac 120  
cttatgtgtg tgetaggtaa ctgacaatc atctacattg tggcgactga gcacagcctg 180  
catgagccca tgtatatatt tctttgcatg ctttcaggca ttgacatcct catctccacc 240  
tcatccatgc ccaaaatgct ggccatcttc tgggtcaatt ccactaccat ccagtttgat 300  
gcttgtctgc tacagatgtt tgccatccac tccttatctg gcatggaatc cacagtgtcg 360  
ctggcctatg cttttgaccg ctatgtggcc atctgtcacc cactgcgcca tggccagcta 420  
cttacgttgc ctctgtgcac caaaattggg ttggctgtcg tgggtcgggg ggctgcaactg 480  
atggcaccct ttctgtcttc catcaagcag ctgcccctct gccgctccaa tatcctttcc 540  
catctctact gccacacca agatgtcatg aagctggcct gtgatgatat cggggtcaat 600  
gtcgtctatg gcttatcgt catcatctcc gccattggcc tggactcact tctcatctcc 660  
ttctcatatc tgcttatctc taagactgtg ttgggcttga cactggaagc ccaggccaag 720  
gcatttggca ctgcgtctc tcatgtgtgt gctgtgttca tattctatgt accttcatt 780  
ggattgtcca tgggtcatcg ctttagcaag cggcgtgact ctccactgcc cgtcatcttg 840  
gccaatatct atctgtcgtt tcctcctgtg ctcaacccea ttgtctatgg agtgaagaca 900  
aaggagattc gacagcgcat ccttcgactt ttccatgtgg ccacacacgc ttcagagccc 960  
taggtgtca 969

<210> 28  
<211> 318  
<212> PRT  
<213> Homo sapiens

<400> 28  
Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile  
1 5 10 15  
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe  
20 25 30  
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile  
35 40 45  
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile  
50 55 60  
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser  
65 70 75 80  
Met Pro Gly Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln  
85 90 95  
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly  
100 105 110  
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala  
115 120 125

Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val  
130 135 140

Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala  
145 150 155 160

Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile  
165 170 175

Leu Ser His Ser Tyr Cys Pro His Gln Asp Val Met Lys Leu Ala Cys  
180 185 190

Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser  
195 200 205

Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile  
210 215 220

Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe  
225 230 235 240

Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro  
245 250 255

Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser  
260 265 270

Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val  
275 280 285

Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg  
290 295 300

Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro  
305 310 315

<210> 29  
<211> 968  
<212> DNA  
<213> Homo sapiens

<400> 29  
ttcttcacga tgggtggatcc caatggcaat gaatccagtg ctacatactt cctcctaata 60  
ggcctccctg gtttagaaga ggctcagttc tgggtggcct tcccatctgt ctcctcttac 120  
cttattgctg tgcctaggtaa cttgacaatc atctacattg tgcggactga gcacagcctg 180  
catgagccca tgtatatatt tctttgcatg ctttcaggca ttgacatcct catctccacc 240  
tcatccatgc ccaaaatgct ggccatcttc tggttcaatt ccactaccat ccagtttgat 300  
gcttgctgc tacagatggt tgccatccac tctttatctg gcattggaatc cacagtgcg 360  
ctggccatgg cttttgacgg ctatgtggcc atctgtcacc cactgcgcca tgcacagta 420  
cttacgttgc ctctgtgcac caaaattgggt gtggctgctg tgggtcgggg ggctgcactg 480  
atggcacccc ttctgtcttc catcaagcag ctgcccctct gccgctccaa tatcctttcc 540  
ctctctact gccacacca agatgtcatg aagctggcct gtgatgatat ccgggtcaat 600  
gtctctatg gcccttatcgt catcatctcc gccattggcc tggactcaat tctcatctcc 660  
ttctcatatc tgccttattct taagactgtg ttgggcttga cactggaagc ccaggccaag 720  
gcatttgcca cttgctgttc tcatgtgtgt gctgtgttca tattctatgt acctttcatt 780  
ggattgtcca tgggtgcatgc ctttagcaag cggcgtgact ctccactgcc cgtcatcttg 840  
gccaatatct atctgctgggt tctctctgtg ctcaacccaa ttgtctatg agtgagaca 900  
aaggagattc gacagcgcat ccttcgactt ttccatgtgg ccacacacgc ttcagagccc 960  
taggtgta 968

<210> 30  
 <211> 318  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
 Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile  
 1 5 10 15  
 Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe  
 20 25 30  
 Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile  
 35 40 45  
 Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile  
 50 55 60  
 Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser  
 65 70 75 80  
 Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln  
 85 90 95  
 Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly  
 100 105 110  
 Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala  
 115 120 125  
 Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val  
 130 135 140  
 Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala  
 145 150 155 160  
 Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile  
 165 170 175  
 Leu Ser His Ser Tyr Cys Pro His Gln Asp Val Met Lys Leu Ala Cys  
 180 185 190  
 Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser  
 195 200 205  
 Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile  
 210 215 220  
 Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe  
 225 230 235 240  
 Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro  
 245 250 255  
 Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser  
 260 265 270  
 Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val  
 275 280 285  
 Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg  
 290 295 300

Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro  
305 310 315

<210> 31  
<211> 980  
<212> DNA  
<213> Homo sapiens

<400> 31  
tgatgctggg tccagcttac aaccacacaa tggaaacccc tgcctccttc ctccctgtgg 60  
gtatcccgag actgcaatct tcacatcttt ggctggctat ctcaactgagt gccatgtaca 120  
tcacagccct gttaggaaac accctcatcg tgactgcaat ctggatggat tccactcggc 180  
atgagcccat gtattgcttt ctgtgtgttc tggctgctgt ggacattgtt atggcctcct 240  
ccgtggtacc caagatgggt agcatcttct gctcgggaga cagctccatc agctttagt 300  
ctgttttcac tcagatgttt ttgttccact tagccacagc tgtggagacg gggctgtgc 360  
tgaccatggc ttgtgaccgc tatgtagcca tctgcaagc tctacactac aagagaattc 420  
tcacgcttca agtggatcgt ggaatgagta tggcgcgtac catcagagct gtacattca 480  
tgactccact gagttggatg atgaatcctc tacctttctg tggctccaat gtggttgtcc 540  
actcctactg taagcacata gctttggcca ggttagcatg tgtgacccc gtgccagca 600  
gtctctacag tctgattggg tctctcttta tgggtgggctc tgatgtggcc ttcatgtgtg 660  
cctcctatat cttaattctc agggcagtat ttgatctctc ctcaaaagact gctcagttga 720  
aagcattaa gacatgtggc tcccatgtgg gggttatggc ttgtactat ctacctggga 780  
tggcatccat ctatgcgccc tgggtggggc aggatatagt gcccttgac acccaagtgc 840  
tgctagctga cctgtacgtg atcatcccag ccactttaaa tcccatcctc tatggcatga 900  
ggaccaaaca attgctggag ggaatatgga gttatctgat gcacttctc tttagaccat 960  
ccaacctggg ttcatgaaca 980

<210> 32  
<211> 324  
<212> PRT  
<213> Homo sapiens

<400> 32  
Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
1 5 10 15  
Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
20 25 30  
Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu  
35 40 45  
Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
50 55 60  
Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
65 70 75 80  
Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
85 90 95  
Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
100 105 110  
Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
115 120 125  
Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
130 135 140  
Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met



145 150 155 160

Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn  
165 170 175

Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala  
180 185 190

Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser  
195 200 205

Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu  
210 215 220

Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys  
225 230 235 240

Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr  
245 250 255

Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile  
260 265 270

Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile  
275 280 285

Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu  
290 295 300

Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His Ser  
305 310 315 320

Asn Leu Gly Ser

<210> 33  
<211> 985  
<212> DNA  
<213> Homo sapiens

<400> 33  
tggtgatgctg ggtccagctt ataaccacac aatggaaacc cctgcctctt tctcctctgt 60  
gggatcccca ggaactgcaat ctccacatct ttggctggct atctcactga gtgccatgta 120  
catcatagcc ctgttaggaa acaccatcat cgtgactgca atctggatgg attccactcg 180  
gcatgagccc atgtattgct ttctgtgtgt tctggctgct gtggacattg ttatggcctc 240  
ctcgggtgta cccaagatgg tgagcatctt ctgctcagga gacagctcaa tcagcttttag 300  
tgcttggttc actcagatgt tttttgtcca cttagccaca gctgtggaga cggggctgct 360  
gctgaccatg gcttttgacc gctatgtagc catctgcaag cctctacact acaagagaat 420  
tctcacgctt caagtgtatg tggaatgag tatggccatc accatcagag ctatcatagc 480  
cataactcca ctgagttgga tgggtagtc tctaccttct tgtggctcca atgtggtgtg 540  
ccactcctac tgtgagcaca tagctttggc cagggttagca tgtgctgacc ccgtgccagc 600  
cagtcctctac agtctgattg gttcctctct tatggtgggc tctgatgtgg ccttcattgc 660  
tgcttctcat actctaattc tcaaggcagt attggtctc tctccaaaga ctgctcagtt 720  
gaaagcatta agcacatgtg gctcccatgt gggggttatg gctttgtact atctacctgg 780  
gatggcatcc atctatgcgg cctgggtggg gcaggatgta gtgcccttgc acacccaagt 840  
cctgctagct caactgtacg tgatcatccc agccacctta aatcccatca tctatggcat 900  
gaggacaaaa caactgcggg agagaatatg gagttatctg atgcatgtcc tctttgacca 960  
ttccaacctg ggttcattgaa caca 985

<210> 34  
<211> 324

<212> PRT

<213> Homo sapiens

<400> 34

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
1 5 10 15

Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
20 25 30

Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Ile  
35 40 45

Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
50 55 60

Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
65 70 75 80

Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
85 90 95

Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
100 105 110

Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
115 120 125

Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
130 135 140

Met Leu Gly Met Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile  
145 150 155 160

Thr Pro Leu Ser Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn  
165 170 175

Val Val Val His Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala  
180 185 190

Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser  
195 200 205

Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu  
210 215 220

Ile Leu Lys Ala Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys  
225 230 235 240

Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr  
245 250 255

Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val  
260 265 270

Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile  
275 280 285

Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu  
290 295 300

Arg Glu Arg Ile Trp Ser Tyr Leu Met His Val Leu Phe Asp His Ser  
305 310 315 320

# Asn Leu Gly Ser

<210> 35  
 <211> 985  
 <212> DNA  
 <213> Homo sapiens

<400> 35  
 tgtgatgctg ggtccagctt ataaccacac aatggaaacc cctgcctcct tctcctctgt 60  
 ggggatccca ggactgcaat ctccacatct ttggctggct atctcactga gtgccatgta 120  
 atcacagcc ctgttaggaa acaccatcat cgtgactgca atctggatgg attccactgc 180  
 gcatgagccc atgtattgct ttctgtgtgt tctggctgct gtggacatcg ttatggcctc 240  
 ctcggtggta cccaagatgg tgagcatctt ctgctcagga gacagctcaa tcagctttag 300  
 tgcttgcttc actcagatgt tttttgtcca cttagccaca gctgtggaga cggggctgct 360  
 gctgaccatg gcttttgacc gctatgtagc catctgcaag cctctacact acaagagaat 420  
 tctcacgcct caagtgatgc tgggaatgag tatggccatc accatcagag ctatcatagc 480  
 cataactcca ctgagttgga tggtagtca tctacctttc tgtggctcca atgtggttgt 540  
 ccactcctac tgtgagcaca tagctttggc caggttagca tgtgctgacc ccgtgccag 600  
 cagtcctcac agtctgattg gtctctctct tatgggtggc tctgatgtgg ccttcattgc 660  
 tgctcctat atcttaattc tcagggcagt atttgatctc tctccaaaga ctgctcagtt 720  
 gaaagcatta agcacatggt gctcccatgt ggggggttat gctttgtact atctacctgg 780  
 gatggcatcc atctatgagg cctggttggg gcaggatata gtgcccttgc acacccaagt 840  
 gctgttagct gcacctgacg tgatcatccc agccacttta aatcccatca tctatggcat 900  
 gaggacccaa caattgctgg agggaaatag gagttatctg atgcacttcc tctttgacca 960  
 ctccaacctg gggtcatgaa caciaa 985

<210> 36  
 <211> 324  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
 1 5 10 15  
 Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
 20 25 30  
 Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Ile  
 35 40 45  
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
 50 55 60  
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
 65 70 75 80  
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
 85 90 95  
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
 100 105 110  
 Ala Val Glu Thr Gly Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
 130 135 140

Met Leu Gly Met Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile  
145 150 155 160

Thr Pro Leu Ser Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn  
165 170 175

Val Val Val His Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala  
180 185 190

Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser  
195 200 205

Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu  
210 215 220

Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys  
225 230 235 240

Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr  
245 250 255

Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile  
260 265 270

Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile  
275 280 285

Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu  
290 295 300

Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His Ser  
305 310 315 320

Asn Leu Gly Ser

<210> 37  
<211> 960  
<212> DNA  
<213> Homo sapiens

<400> 37  
gccatgctca cttttcataa tgtctgctca gtacccagct ccttctgggt cactggcctc 60  
ccagggtcgg agtcctcaca cgtctggctc tccatccctc ttgggtccat gtacctgggtg 120  
gctgtggtgg ggaatgtgac catctcggct gtggtaaaaga tagaacgcag cctgcaccag 180  
cccatgtact ttttcttggt catgttgggt gccattgacc tgggttctgtc tacttccact 240  
atacccaaac ttctgggaat ctctcgggtc ggtgcttggt acattggcct ggaagcctgc 300  
ttggggccaaa tgttctctat ccactgcttt gccactgttg agtcaggcat ctctcctgcc 360  
atggcttttg atcgctacgt ggccatctgc aacccaactac gtcatagcat ggtgctcact 420  
tatacagtgg tgggtcgttt ggggcttggt tctctcctcc ggggtgttct ctacattgga 480  
cctctgcctc tgatgatccg cctgcggctg cccctttata aaacccatgt tatctccacc 540  
tctactgttg agcacatggc ttagttggcc ttgacatgt gcgacagcag ggtcaataat 600  
gtctatgggc tgagcatcgg ctttctgggt ttgatccctgg actcagtggc tattgttcca 660  
tcctatgtga tgattttcag ggccgtgatg ggggttagcca ctccctgaggc taggcttaaa 720  
accctgggga catgcgcttc tcacctgtgt gccatcctga tcttttatgt tcccattgct 780  
gtttcttccc tgattcacgg atttggtcag tgtgtgcctc ctccagtgca cactctgctg 840  
gccaactctc atctcctcat tctccaatc ctcaatccca ttgtctatgc tgttcgcacc 900  
aagcagatcc gagagagcct tctccaataa ccaaggatag aaatgaagat tagatgatta 960

<210> 38  
<211> 317

<212> PRT  
<213> Homo sapiens

<400> 38

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu  
1 5 10 15  
Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro  
20 25 30  
Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu  
35 40 45  
Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe  
50 55 60  
Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile  
65 70 75 80  
Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu  
85 90 95  
Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val  
100 105 110  
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
115 120 125  
Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly  
130 135 140  
Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro  
145 150 155 160  
Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val  
165 170 175  
Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys  
180 185 190  
Gly Asp Ser Arg Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu  
195 200 205  
Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile  
210 215 220  
Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr  
225 230 235 240  
Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Val  
245 250 255  
Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro  
260 265 270  
Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro  
275 280 285  
Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu  
290 295 300  
Ser Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg  
305 310 315

<210> 39  
 <211> 997  
 <212> DNA  
 <213> Homo sapiens

<400> 39  
 agccatgctc acttttcata atgtctgctc agtaccagc tctctctggc tcaactggcat 60  
 cccagggctg gagtccctac acgtctggct ctcacatccc ttgggtccca tgtacctggg 120  
 ggctgtgggtg ggggaatgtga ccatcctggc tgtggtaaa atagaacgca gcctgcacca 180  
 gcccatgtac tttttctgtg gcatgttggc tgccattgac ctggttctgt ctacttcac 240  
 tatacccaaa ctctctgggaa tcttctgggt cgggtctgtg gacattggcc tggatgctg 300  
 ctggggccaa atgttctcta tccactgctt tgccactggt gagtcaaggca tcttctctgc 360  
 catggctttt gatcgctatg tggccatctg caaccacta cgtcatagca tgggtgctac 420  
 ttatacagtg gtgggtcggt tggggcttgt tctctctc cggggtgttc tctacattgg 480  
 acctctgcct ctgatgatcc gccctgggct gccctttat aaaacccatg ttacttccca 540  
 ctctactgtg gagcacatgg ctgtagtgtc ctlgacatgt ggcgacagca ggggcaataa 600  
 tgtctatggg ctgagcatcg gctttctggg gttgactctg gactcagtggt ctattgctac 660  
 atcctatgtg atgattttca gggccgtgat ggggttagcc actcctgagg ctaggcttaa 720  
 aaccctgggg acatgcgctt ctcacctctg tgccatcctg atcttttatg ttccattgc 780  
 tgtttcttcc ctgattcacc gatttggtca gtgtgtgcct cctccagtc cactctgct 840  
 ggccaacttc tatctctca tctctccaat cctcaatccc attgtctatg ctgttgcac 900  
 caagcagatc cgagagaggg ttctccaaat accaaggata gaaatgaaga ttagatgatt 960  
 actattttct tctctctcaa ataagctcat ggagaag 997

<210> 40  
 <211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 40  
 Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu  
 1 5 10 15  
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro  
 20 25 30  
 Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu  
 35 40 45  
 Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe  
 50 55 60  
 Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile  
 65 70 75 80  
 Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu  
 85 90 95  
 Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val  
 100 105 110  
 Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly  
 130 135 140  
 Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro  
 145 150 155 160

Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val  
 165 170 175  
 Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys  
 180 185 190  
 Gly Asp Ser Arg Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu  
 195 200 205  
 Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile  
 210 215 220  
 Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr  
 225 230 235 240  
 Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Val  
 245 250 255  
 Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro  
 260 265 270  
 Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro  
 275 280 285  
 Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu  
 290 295 300  
 Arg Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg  
 305 310 315

<210> 41  
 <211> 997  
 <212> DNA  
 <213> Homo sapiens

<400> 41  
 agccatgctc acttttcata atgtctgctc agtaccacgc tccttctggc tcactggcat 60  
 cccagggtcg gactccctac acgtctggct ctccatcccc ttgggtccca tgtactgggt 120  
 ggctgtgggt gggaaatgta ccatctctggc tgtggtaaa atagaacgca gccctgcacca 180  
 gcccatgtac tttttcttgt gcatgttggc tgccattgac ctggttctgt ctactccac 240  
 tatacccaaa ctctcgggaa tcttctgggt cggtgcttgt gacattggcc tggatggcctg 300  
 ctggggccaa atgttcctta tccactgctt tgccactgtt gactcaggca tcttctctgc 360  
 catggctttt gatcgctacg tggccatctg caaccaccta cgctcatagca tggctgctcac 420  
 ttatacagtg gtgggtcggt tggggcttgt ttctctctcc cggggtggtc tctacattgg 480  
 acctctgcct ctgatgatcc gcctcgggct gcccttttat aaaccccatg ttatctccca 540  
 ctctactgtg gagcacatgg ctgtagtgtc cttgacatgt ggcgacagca gggtaataaa 600  
 tgtctatggg ctgagcatcg gctttctggg gttgatcctg gactcagttg ctattgctgc 660  
 atctcatgtg atgattttca gggccgtgat ggggttagcc actcctgagg ctaggcttaa 720  
 aacctggggg acatgcgcct ctcacctctg tgccatcctg atcttttatg ttcccaattg 780  
 tgtttcttcc ctgattcacc gatttggtca gtgtgtgctc cctccagtc acactctgct 840  
 ggccaacttc tatctcctca ttctccaat cctcaatccc attgtctatg ctgttcgcac 900  
 caagcagatc cgagagaggc ttctccaat accaaggata gaaatgaaga ttagatgatt 960  
 actattttct tctctctcaa ataagctcat ggagaag 997

<210> 42  
 <211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 42  
 Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu

| 1   | 5   | 10  | 15  |
|---|---|-----|-----|
| Thr Gly Ile Pro   | Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro |     |     |
|   | 20  | 25  | 30  |
| Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu |   |     |     |
|   | 35  | 40  | 45  |
| Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe |   |     |     |
|   | 50  | 55  | 60  |
| Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile |   |     |     |
|   | 65  | 70  | 75  |
| Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu |   |     |     |
|   | 85  | 90  | 95  |
| Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val |   |     |     |
|   | 100   | 105 | 110 |
| Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile |   |     |     |
|   | 115   | 120 | 125 |
| Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly |   |     |     |
|   | 130   | 135 | 140 |
| Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro |   |     |     |
|   | 145   | 150 | 155 |
| Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val |   |     |     |
|   | 165   | 170 | 175 |
| Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys |   |     |     |
|   | 180   | 185 | 190 |
| Gly Asp Ser Gly Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu |   |     |     |
|   | 195   | 200 | 205 |
| Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile |   |     |     |
|   | 210   | 215 | 220 |
| Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr |   |     |     |
|   | 225   | 230 | 235 |
| Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Ile |   |     |     |
|   | 245   | 250 | 255 |
| Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro |   |     |     |
|   | 260   | 265 | 270 |
| Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro |   |     |     |
|   | 275   | 280 | 285 |
| Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu |   |     |     |
|   | 290   | 295 | 300 |
| Arg Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg             |   |     |     |
|   | 305   | 310 | 315 |

<210> 43  
 <211> 387  
 <212> PRT



<213> Homo sapiens

<400> 43

Met Asn Arg His His Leu Gln Asp His Phe Leu Glu Ile Asp Lys Lys  
1 5 10 15  
Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro  
20 25 30  
Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala  
35 40 45  
Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile  
50 55 60  
Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Ile Ile Cys Leu  
65 70 75 80  
Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Asn Phe Gly  
85 90 95  
Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln  
100 105 110  
Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg  
115 120 125  
Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala  
130 135 140  
Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val  
145 150 155 160  
His Leu Leu Lys Lys Lys Leu Leu Ile Gln Asn Gly Pro Ala Asn Val  
165 170 175  
Cys Ile Ser Phe Ser Ile Cys His Thr Phe Arg Trp His Glu Ala Met  
180 185 190  
Phe Leu Leu Glu Phe Leu Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser  
195 200 205  
Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala  
210 215 220  
Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe  
225 230 235 240  
Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp  
245 250 255  
Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val  
260 265 270  
Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met  
275 280 285  
Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe  
290 295 300  
Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu  
305 310 315 320

Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn  
 325 330 335

Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro  
 340 345 350

Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Asn Asn His Ser Lys Lys  
 355 360 365

Gly His Cys His Gln Glu Pro Ala Ser Leu Glu Lys Gln Leu Gly Cys  
 370 375 380

Cys Ile Glu  
 385

<210> 44  
 <211> 360  
 <212> PRT  
 <213> Mus musculus

<400> 44  
 Met Ser Lys Ser Asp His Phe Leu Val Ile Asn Gly Lys Asn Cys Cys  
 1 5 10 15

Val Phe Arg Asp Glu Asn Ile Ala Lys Val Leu Pro Pro Val Leu Gly  
 20 25 30

Leu Glu Phe Val Phe Gly Leu Leu Gly Asn Gly Leu Ala Leu Trp Ile  
 35 40 45

Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile Phe Leu Phe  
 50 55 60

Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu Pro Phe Leu  
 65 70 75 80

Thr Asp Asn Tyr Val His Asn Trp Asp Trp Arg Phe Gly Gly Ile Pro  
 85 90 95

Cys Arg Val Met Leu Phe Met Leu Ala Met Asn Arg Gln Gly Ser Ile  
 100 105 110

Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg Val Val His  
 115 120 125

Pro His His Phe Leu Asn Lys Ile Ser Asn Arg Thr Ala Ala Ile Ile  
 130 135 140

Ser Cys Phe Leu Trp Gly Leu Thr Ile Gly Leu Thr Val His Leu Leu  
 145 150 155 160

Tyr Thr Asn Met Met Thr Lys Asn Gly Glu Ala Tyr Leu Cys Ser Ser  
 165 170 175

Phe Ser Ile Cys Tyr Asn Phe Arg Trp His Asp Ala Met Phe Leu Leu  
 180 185 190

Glu Phe Phe Leu Pro Leu Ala Ile Ile Leu Phe Cys Ser Gly Arg Ile  
 195 200 205

Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala Lys Ile Lys  
 210 215 220

Arg Ala Ile Asn Phe Ile Met Val Val Ala Ile Val Phe Ile Ile Cys  
225 230 235 240

Phe Leu Pro Ser Val Ala Val Arg Ile Arg Ile Phe Trp Leu Leu Tyr  
245 250 255

Lys Tyr Asn Val Arg Asn Cys Asp Ile Tyr Ser Ser Val Asp Leu Ala  
260 265 270

Phe Phe Thr Thr Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro  
275 280 285

Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe Phe Ser Thr  
290 295 300

Cys Ile Asn Arg Cys Leu Arg Lys Lys Thr Leu Gly Glu Pro Asp Asn  
305 310 315 320

Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Ser Thr Thr Arg  
325 330 335

Ser Ile Pro Gly Ala Leu Met Ala Asp Pro Ser Glu Pro Gly Ser Pro  
340 345 350

Pro Tyr Leu Ala Ser Thr Ser Arg  
355 360

<210> 45

<211> 319

<212> PRT

<213> Mus musculus

<400> 45

Met Glu His Thr Asn Cys Ser Ala Ala Ser Thr Val Val Glu Thr Ala  
1 5 10 15

Val Gly Thr Met Leu Thr Leu Glu Cys Val Leu Gly Leu Met Gly Asn  
20 25 30

Ala Val Ala Leu Trp Thr Phe Phe Tyr Arg Leu Lys Val Trp Lys Pro  
35 40 45

Tyr Ala Val Tyr Leu Phe Asn Leu Val Val Ala Asp Leu Leu Leu Ala  
50 55 60

Thr Ser Val Pro Phe Phe Ala Ala Phe Tyr Leu Lys Gly Lys Thr Trp  
65 70 75 80

Lys Leu Gly His Met Pro Cys Gln Leu Leu Leu Phe Leu Leu Ala Phe  
85 90 95

Ser Cys Gly Val Gly Val Ala Phe Leu Met Thr Val Ala Leu Asp Arg  
100 105 110

Tyr Leu His Val Val His Pro Arg Leu Arg Val Asn Leu Leu Ser Leu  
115 120 125

Arg Ala Ala Trp Gly Ile Ser Ser Leu Ile Trp Leu Leu Met Val Val  
130 135 140

Leu Thr Pro Gln Asn Leu Leu Thr Cys Arg Thr Thr Gln Asn Ser Thr  
35



Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His  
 130 135 140  
 Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val  
 145 150 155 160  
 Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu  
 165 170 175  
 Phe Tyr Ser Gly Thr Gly Val Arg Arg Asn Lys Thr Ile Thr Cys Tyr  
 180 185 190  
 Asp Thr Thr Ala Asp Glu Tyr Leu Arg Ser Tyr Phe Val Tyr Ser Met  
 195 200 205  
 Cys Thr Thr Val Phe Met Phe Cys Ile Pro Phe Ile Val Ile Leu Gly  
 210 215 220  
 Cys Tyr Gly Leu Ile Val Lys Ala Leu Ile Tyr Lys Asp Leu Asp Asn  
 225 230 235 240  
 Ser Pro Leu Arg Arg Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr  
 245 250 255  
 Val Phe Ala Val Ser Tyr Leu Pro Phe His Val Met Lys Thr Leu Asn  
 260 265 270  
 Leu Arg Ala Arg Leu Asp Phe Gln Thr Pro Gln Met Cys Ala Phe Asn  
 275 280 285  
 Asp Lys Val Tyr Ala Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu  
 290 295 300  
 Asn Ser Cys Val Asp Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe  
 305 310 315 320  
 Arg Arg Arg Leu Ser Arg Ala Thr Arg Lys Ser Ser Arg Arg Ser Glu  
 325 330 335  
 Pro Asn Val Gln Ser Lys Ser Glu Glu Met Thr Leu Asn Ile Leu Thr  
 340 345 350  
 Glu Tyr Lys Gln Asn Gly Asp Thr Ser Leu  
 355 360

<210> 47  
 <211> 362  
 <212> PRT  
 <213> Meleagris gallopavo

<400> 47  
 Met Thr Glu Ala Leu Ile Ser Ala Ala Leu Asn Gly Thr Gln Pro Glu  
 1 5 10 15  
 Leu Leu Ala Gly Gly Trp Ala Ala Gly Asn Ala Ser Thr Lys Cys Ser  
 20 25 30  
 Leu Thr Lys Thr Gly Phe Gln Phe Tyr Tyr Leu Pro Thr Val Tyr Ile  
 35 40 45  
 Leu Val Phe Ile Thr Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met  
 50 55 60

Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe  
65 70 75 80  
Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu  
85 90 95  
Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met  
100 105 110  
Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile  
115 120 125  
Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His  
130 135 140  
Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val  
145 150 155 160  
Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu  
165 170 175  
Phe Tyr Ser Gly Thr Gly Val Arg Arg Asn Lys Thr Ile Thr Cys Tyr  
180 185 190  
Asp Thr Thr Ala Asp Glu Tyr Leu Arg Ser Tyr Phe Val Tyr Ser Met  
195 200 205  
Cys Thr Thr Val Phe Met Phe Cys Ile Pro Phe Ile Val Ile Leu Gly  
210 215 220  
Cys Tyr Gly Leu Ile Val Lys Ala Leu Ile Tyr Lys Asp Leu Asp Asn  
225 230 235 240  
Ser Pro Leu Arg Arg Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr  
245 250 255  
Val Phe Ala Val Ser Tyr Leu Pro Phe His Val Met Lys Thr Leu Asn  
260 265 270  
Leu Arg Ala Arg Leu Asp Phe Gln Thr Pro Gln Met Cys Ala Phe Asn  
275 280 285  
Asp Lys Val Tyr Ala Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu  
290 295 300  
Asn Ser Cys Val Asp Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe  
305 310 315 320  
Arg Arg Arg Leu Ser Arg Ala Thr Arg Lys Ser Ser Arg Arg Ser Glu  
325 330 335  
Pro Asn Val Gln Ser Lys Ser Glu Glu Met Thr Leu Asn Ile Leu Thr  
340 345 350  
Glu Tyr Lys Gln Asn Gly Asp Thr Ser Leu  
355 360

<210> 48  
<211> 469  
<212> PRT  
<213> Homo sapiens

<400> 48

Met Gln Met Ala Asp Ala Ala Thr Ile Ala Thr Met Asn Lys Ala Ala  
1 5 10 15

Gly Gly Asp Lys Leu Ala Glu Leu Phe Ser Leu Val Pro Asp Leu Leu  
20 25 30

Glu Ala Ala Asn Thr Ser Gly Asn Ala Ser Leu Gln Leu Pro Asp Leu  
35 40 45

Trp Trp Glu Leu Gly Leu Glu Leu Pro Asp Gly Ala Pro Pro Gly His  
50 55 60

Pro Pro Gly Ser Gly Gly Ala Glu Ser Ala Asp Thr Glu Ala Arg Val  
65 70 75 80

Arg Ile Leu Ile Ser Val Val Tyr Trp Val Val Cys Ala Leu Gly Leu  
85 90 95

Ala Gly Asn Leu Leu Val Leu Tyr Leu Met Lys Ser Met Gln Gly Trp  
100 105 110

Arg Lys Ser Ser Ile Asn Leu Phe Val Thr Asn Leu Ala Leu Thr Asp  
115 120 125

Phe Gln Phe Val Leu Thr Leu Pro Phe Trp Ala Val Glu Asn Ala Leu  
130 135 140

Asp Phe Lys Trp Pro Phe Gly Lys Ala Met Cys Lys Ile Val Ser Met  
145 150 155 160

Val Thr Ser Met Asn Met Tyr Ala Ser Val Phe Phe Leu Thr Ala Met  
165 170 175

Ser Val Thr Arg Tyr His Ser Val Ala Ser Ala Leu Lys Ser His Arg  
180 185 190

Thr Arg Gly His Gly Arg Gly Asp Cys Cys Gly Arg Ser Leu Gly Asp  
195 200 205

Ser Cys Cys Phe Ser Ala Lys Ala Leu Cys Val Trp Ile Trp Ala Leu  
210 215 220

Ala Ala Leu Ala Ser Leu Pro Ser Ala Ile Phe Ser Thr Thr Val Lys  
225 230 235 240

Val Met Gly Glu Glu Leu Cys Leu Val Arg Phe Pro Asp Lys Leu Leu  
245 250 255

Gly Arg Asp Arg Gln Phe Trp Leu Gly Leu Tyr His Ser Gln Lys Val  
260 265 270

Leu Leu Gly Phe Val Leu Pro Leu Gly Ile Ile Ile Leu Cys Tyr Leu  
275 280 285

Leu Leu Val Arg Phe Ile Ala Asp Arg Arg Ala Ala Gly Thr Lys Gly  
290 295 300

Gly Ala Ala Val Ala Gly Gly Arg Pro Thr Gly Ala Ser Ala Arg Arg  
305 310 315 320

Leu Ser Lys Val Thr Lys Ser Val Thr Ile Val Val Leu Ser Phe Phe

325                      330                      335  
 Leu Cys Trp Leu Pro Asn Gln Ala Leu Thr Thr Trp Ser Ile Leu Ile  
                          340                      345                      350  
 Lys Phe Asn Ala Val Pro Phe Ser Gln Glu Tyr Phe Leu Cys Gln Val  
                          355                      360                      365  
 Tyr Ala Phe Pro Val Ser Val Cys Leu Ala His Ser Asn Ser Cys Leu  
                          370                      375                      380  
 Asn Pro Val Leu Tyr Cys Leu Val Arg Arg Glu Phe Arg Lys Ala Leu  
                          385                      390                      395                      400  
 Lys Ser Leu Leu Trp Arg Ile Ala Ser Pro Ser Ile Thr Ser Met Arg  
                          405                      410                      415  
 Pro Phe Thr Ala Thr Thr Lys Pro Glu His Glu Asp Gln Gly Leu Gln  
                          420                      425                      430  
 Ala Pro Ala Pro Pro His Ala Ala Ala Glu Pro Asp Leu Leu Tyr Tyr  
                          435                      440                      445  
 Pro Pro Gly Val Val Val Tyr Ser Gly Gly Arg Tyr Asp Leu Leu Pro  
                          450                      455                      460  
 Ser Ser Ser Ala Tyr  
 465  
 <210> 49  
 <211> 359  
 <212> PRT  
 <213> Cavia porcellus  
 <400> 49  
 Met Ile Leu Asn Ser Ser Thr Gln Asp Gly Ile Lys Arg Ile Gln Asp  
                          1                      5                      10                      15  
 Asp Cys Pro Lys Asp Gly Arg His Ser Tyr Ile Phe Val Met Ile Pro  
                          20                      25                      30  
 Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
                          35                      40                      45  
 Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
                          50                      55                      60  
 Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Ile Cys Phe Leu Leu Thr  
                          65                      70                      75                      80  
 Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
                          85                      90                      95  
 Gly Asn Tyr Met Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
                          100                      105                      110  
 Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
                          115                      120                      125  
 Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
                          130                      135                      140



Ala Lys Val Thr Cys Val Ile Ile Trp Leu Met Ala Gly Leu Ala Ser  
 145 150 155 160  
 Leu Pro Ala Val Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
 165 170 175  
 Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
 180 185 190  
 Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Met Phe Pro Phe  
 195 200 205  
 Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
 210 215 220  
 Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
 225 230 235 240  
 Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Val Pro His  
 245 250 255  
 Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile His  
 260 265 270  
 Asp Cys Lys Ile Ser Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
 275 280 285  
 Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
 290 295 300  
 Leu Gly Lys Lys Phe Lys Lys Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
 305 310 315 320  
 Pro Pro Lys Ala Lys Ser His Ser Thr Leu Ser Thr Lys Met Ser Thr  
 325 330 335  
 Leu Ser Tyr Arg Pro Ser Asn Asn Val Ser Ser Ser Ala Lys Lys Pro  
 340 345 350  
 Val Gln Cys Phe Glu Val Glu  
 355

<210> 50

<211> 359

<212> PRT

<213> *Cavia porcellus*

<400> 50

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
 1 5 10 15  
 Asp Cys Pro Lys Ala Gly Arg His Ser Tyr Ile Phe Val Met Ile Pro  
 20 25 30  
 Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
 35 40 45  
 Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
 50 55 60  
 Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Ile Cys Phe Leu Leu Thr  
 65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
 85 90 95  
 Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
 100 105 110  
 Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
 115 120 125  
 Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
 130 135 140  
 Ala Lys Val Thr Cys Val Ile Ile Trp Leu Met Ala Gly Leu Ala Ser  
 145 150 155 160  
 Leu Pro Ala Val Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
 165 170 175  
 Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
 180 185 190  
 Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Met Phe Pro Phe  
 195 200 205  
 Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
 210 215 220  
 Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
 225 230 235 240  
 Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Val Pro His  
 245 250 255  
 Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile His  
 260 265 270  
 Asp Cys Lys Ile Ser Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
 275 280 285  
 Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
 290 295 300  
 Leu Gly Lys Lys Phe Lys Lys Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
 305 310 315 320  
 Pro Pro Lys Ala Lys Ser His Ser Thr Leu Ser Thr Lys Met Ser Thr  
 325 330 335  
 Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Ala Lys Lys Pro  
 340 345 350  
 Val Gln Cys Phe Glu Val Glu  
 355

<210> 51  
 <211> 359  
 <212> PRT  
 <213> Mus musculus

<400> 51  
 Met Ala Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp

|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Asp Cys Pro Arg Ala Gly Arg His Ser Tyr Ile Phe Val Met Ile Pro | 20  | 25  | 30  |
| Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu | 35  | 40  | 45  |
| Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser | 50  | 55  | 60  |
| Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr | 65  | 70  | 75  |
| Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe | 85  | 90  | 95  |
| Gly Asn His Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu | 100 | 105 | 110 |
| Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu | 115 | 120 | 125 |
| Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val | 130 | 135 | 140 |
| Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Met Ala Gly Leu Ala Ser | 145 | 150 | 155 |
| Leu Pro Ala Val Ile His Arg Asn Val Tyr Phe Ile Glu Asn Thr Asn | 165 | 170 | 175 |
| Ile Thr Val Cys Ala Phe His Tyr Glu Ser Arg Asn Ser Thr Leu Pro | 180 | 185 | 190 |
| Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe | 195 | 200 | 205 |
| Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys | 210 | 215 | 220 |
| Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Arg | 225 | 230 | 235 |
| Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Val Pro His     | 245 | 250 | 255 |
| Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Val Ile His | 260 | 265 | 270 |
| Asp Cys Lys Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile | 275 | 280 | 285 |
| Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe | 290 | 295 | 300 |
| Leu Gly Lys Lys Phe Lys Lys Tyr Phe Leu Gln Leu Leu Lys Tyr Ile | 305 | 310 | 315 |
| Pro Pro Lys Ala Lys Ser His Ser Ser Leu Ser Thr Lys Met Ser Thr | 325 | 330 | 335 |
| Leu Ser Tyr Arg Pro Ser Asp Asn Met Ser Ser Ala Ala Lys Lys Pro |     |     |     |

Ala Ser Cys Ser Glu Val Glu  
355

<210> 52  
<211> 359  
<212> PRT  
<213> Mus musculus

<400> 52  
Met Ala Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
1 5 10 15

Asp Cys Pro Arg Ala Gly Arg His Ser Tyr Ile Phe Val Met Ile Pro  
20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
85 90 95

Gly Asn His Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Met Ala Gly Leu Ala Ser  
145 150 155 160

Leu Pro Ala Val Ile His Arg Asn Val Tyr Phe Ile Glu Asn Thr Asn  
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Arg Asn Ser Thr Leu Pro  
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Arg  
225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Val Pro His  
245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Val Ile His  
260 265 270

Asp Cys Lys Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
 275 280 285  
 Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
 290 295 300  
 Leu Gly Lys Lys Phe Lys Lys Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
 305 310 315 320  
 Pro Pro Lys Ala Lys Ser His Ser Ser Leu Ser Thr Lys Met Ser Thr  
 325 330 335  
 Leu Ser Tyr Arg Pro Ser Asp Asn Met Ser Ser Ala Ala Lys Lys Pro  
 340 345 350  
 Ala Ser Cys Ser Glu Val Glu  
 355

<210> 53  
 <211> 318  
 <212> PRT  
 <213> Mus musculus  
 <220>  
 <221> VARIANT  
 <222> (286)  
 <223> Wherein Xaa is any amino acid.  
 <400> 53  
 Met Ser Pro Gly Asn Ser Ser Trp Ile His Pro Ser Ser Phe Leu Leu  
 1 5 10 15  
 Leu Gly Ile Pro Gly Leu Glu Glu Leu Gln Phe Trp Leu Gly Leu Pro  
 20 25 30  
 Phe Gly Thr Val Tyr Leu Ile Ala Val Leu Gly Asn Val Ile Ile Leu  
 35 40 45  
 Phe Val Ile Tyr Leu Glu His Ser Leu His Gln Pro Met Phe Tyr Leu  
 50 55 60  
 Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Ser Thr Ala Thr Val  
 65 70 75 80  
 Pro Arg Ala Leu Gly Ile Phe Trp Phe Gly Phe His Lys Ile Ala Phe  
 85 90 95  
 Arg Asp Cys Val Ala Gln Met Phe Phe Ile His Leu Phe Thr Gly Ile  
 100 105 110  
 Glu Thr Phe Met Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Arg Tyr Asn Thr Ile Leu Thr Asn Arg Thr Ile Cys  
 130 135 140  
 Ile Ile Val Gly Val Gly Leu Phe Lys Asn Phe Ile Leu Val Phe Pro  
 145 150 155 160  
 Leu Ile Phe Leu Ile Leu Arg Leu Ser Phe Cys Gly His Asn Ile Ile  
 165 170 175

Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Val  
180 185 190

Ser Ile Lys Val Asn Val Leu Phe Gly Leu Ile Leu Ile Ser Met Ile  
195 200 205

Leu Leu Asp Val Val Leu Ser Ala Leu Ser Tyr Ala Lys Ile Leu His  
210 215 220

Ala Val Phe Lys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn  
225 230 235 240

Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Phe Thr Pro Ala  
245 250 255

Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Arg Tyr  
260 265 270

Ile His Ile Leu Leu Ala Asn Leu Tyr Val Ile Ile Pro Xaa Ala Leu  
275 280 285

Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Asp Arg Ala  
290 295 300

Val Thr Ile Leu Cys Asn Glu Val Gly Gln Leu Ala Asp Asp  
305 310 315

<210> 54

<211> 339

<212> PRT

<213> Mus musculus

<400> 54

Met Pro Glu Lys Met Leu Ser Lys Leu Ile Ala Tyr Leu Leu Leu Ile  
1 5 10 15

Glu Ser Cys Arg Gln Thr Ala Gln Leu Val Lys Gly Arg Arg Ile Trp  
20 25 30

Val Asp Ser Arg Pro His Trp Pro Asn Thr Thr His Tyr Arg Glu Leu  
35 40 45

Glu Asp Gln His Val Trp Ile Ala Ile Pro Phe Cys Ser Met Tyr Ile  
50 55 60

Leu Ala Leu Val Gly Asn Gly Thr Ile Leu Tyr Ile Ile Ile Thr Asp  
65 70 75 80

Arg Ala Leu His Glu Pro Met Tyr Leu Phe Leu Cys Leu Leu Ser Ile  
85 90 95

Thr Asp Leu Val Leu Cys Ser Thr Thr Leu Pro Lys Met Leu Ala Ile  
100 105 110

Phe Trp Leu Arg Ser His Val Ile Ser Tyr His Gly Cys Leu Thr Gln  
115 120 125

Met Phe Phe Val His Ala Val Phe Ala Thr Glu Ser Ala Val Leu Leu  
130 135 140

Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu His Tyr  
145 150 155 160

Thr Ser Ile Leu Asn Ala Val Val Ile Gly Lys Ile Gly Leu Ala Cys  
 165 170 175  
 Val Thr Arg Gly Leu Leu Phe Val Phe Pro Phe Val Ile Leu Ile Glu  
 180 185 190  
 Arg Leu Pro Phe Cys Gly His His Ile Ile Pro His Thr Tyr Cys Glu  
 195 200 205  
 His Met Gly Ile Ala Lys Leu Ala Cys Ala Ser Ile Lys Pro Asn Thr  
 210 215 220  
 Ile Tyr Gly Leu Thr Val Ala Leu Ser Val Thr Gly Met Asp Val Val  
 225 230 235 240  
 Leu Ile Ala Thr Ser Tyr Ile Leu Ile Leu Gln Ala Val Leu Arg Leu  
 245 250 255  
 Pro Ser Lys Asp Ala Gln Phe Arg Ala Phe Ser Thr Cys Gly Ala His  
 260 265 270  
 Ile Cys Val Ile Leu Val Phe Tyr Ile Pro Ala Phe Phe Ser Phe Phe  
 275 280 285  
 Thr His Arg Phe Gly His His Val Pro Pro Gln Val His Ile Ile Leu  
 290 295 300  
 Ala Asn Leu Tyr Leu Leu Val Pro Pro Val Leu Asn Pro Leu Val Tyr  
 305 310 315 320  
 Gly Ile Asn Thr Lys Gln Ile Arg Leu Arg Ile Leu Asp Phe Phe Val  
 325 330 335  
 Lys Arg Arg

<210> 55  
 <211> 318  
 <212> PRT  
 <213> Homo sapiens

<400> 55  
 Met Ser Asp Ser Asn Leu Ser Asp Asn His Leu Pro Asp Thr Phe Phe  
 1 5 10 15  
 Leu Thr Gly Ile Pro Gly Leu Glu Ala Ala His Phe Trp Ile Ala Ile  
 20 25 30  
 Pro Phe Cys Ala Met Tyr Leu Val Ala Leu Val Gly Asn Ala Ala Leu  
 35 40 45  
 Ile Leu Val Ile Ala Met Asp Asn Ala Leu His Ala Pro Met Tyr Leu  
 50 55 60  
 Phe Leu Cys Leu Leu Ser Leu Thr Asp Leu Ala Leu Ser Ser Thr Thr  
 65 70 75 80  
 Val Pro Lys Met Leu Ala Ile Leu Trp Leu His Ala Gly Glu Ile Ser  
 85 90 95  
 Phe Gly Gly Cys Leu Ala Gln Met Phe Cys Val His Ser Ile Tyr Ala

|   |     |     |
|---|-----|-----|
| 100   | 105 | 110 |
| Leu Glu Ser Ser Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala |     |     |
| 115   | 120 | 125 |
| Ile Cys Asn Pro Leu Arg Tyr Thr Thr Ile Leu Asn His Ala Val Ile |     |     |
| 130   | 135 | 140 |
| Gly Arg Ile Gly Phe Val Gly Leu Phe Arg Ser Val Ala Ile Val Ser |     |     |
| 145   | 150 | 155 |
| Pro Phe Ile Phe Leu Leu Arg Arg Leu Pro Tyr Cys Gly His Arg Val |     |     |
| 165   | 170 | 175 |
| Met Thr His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys |     |     |
| 180   | 185 | 190 |
| Ala Asn Ile Thr Val Asn Ile Val Tyr Gly Leu Thr Val Ala Leu Leu |     |     |
| 195   | 200 | 205 |
| Ala Met Gly Leu Asp Ser Ile Leu Ile Ala Ile Ser Tyr Gly Phe Ile |     |     |
| 210   | 215 | 220 |
| Leu His Ala Val Phe His Leu Pro Ser His Asp Ala Gln His Lys Ala |     |     |
| 225   | 230 | 235 |
| Leu Ser Thr Cys Gly Ser His Ile Gly Ile Ile Leu Val Phe Tyr Ile |     |     |
| 245   | 250 | 255 |
| Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly His His Glu Val |     |     |
| 260   | 265 | 270 |
| Pro Lys His Val His Ile Phe Leu Ala Asn Leu Tyr Val Leu Val Pro |     |     |
| 275   | 280 | 285 |
| Pro Val Leu Asn Pro Ile Leu Tyr Gly Ala Arg Thr Lys Glu Ile Arg |     |     |
| 290   | 295 | 300 |
| Ser Arg Leu Leu Lys Leu Leu His Leu Gly Lys Thr Ser Ile         |     |     |
| 305   | 310 | 315 |

<210> 56  
 <211> 321  
 <212> PRT  
 <213> Mus musculus

<400> 56  
 Met Asn Ser Lys Ala Ser Met Leu Gly Thr Asn Phe Thr Ile Ile His  
 1 5 10 15  
 Pro Thr Val Phe Ile Leu Leu Gly Ile Pro Gly Leu Glu Gln Tyr His  
 20 25 30  
 Thr Trp Leu Ser Ile Pro Phe Cys Leu Met Tyr Ile Ala Ala Val Leu  
 35 40 45  
 Gly Asn Gly Ala Leu Ile Leu Val Val Leu Ser Glu Arg Thr Leu His  
 50 55 60  
 Glu Pro Met Tyr Val Phe Leu Ser Met Leu Ala Gly Thr Asp Ile Leu  
 65 70 75 80



Leu Ser Thr Thr Thr Val Pro Lys Thr Leu Ala Ile Phe Trp Phe His  
 85 90 95  
 Ala Gly Glu Ile Pro Phe Asp Ala Cys Ile Ala Gln Met Phe Phe Ile  
 100 105 110  
 His Val Ala Phe Val Ala Glu Ser Gly Ile Leu Leu Ala Met Ala Phe  
 115 120 125  
 Asp Arg Tyr Val Ala Ile Cys Thr Pro Leu Arg Tyr Ser Ala Val Leu  
 130 135 140  
 Thr Pro Met Ala Ile Gly Lys Met Thr Leu Ala Ile Trp Gly Arg Ser  
 145 150 155 160  
 Ile Gly Thr Ile Phe Pro Ile Ile Phe Leu Leu Lys Arg Leu Ser Tyr  
 165 170 175  
 Cys Arg Thr Asn Val Ile Pro His Ser Tyr Cys Glu His Ile Gly Val  
 180 185 190  
 Ala Arg Leu Ala Cys Ala Asp Ile Thr Val Asn Ile Trp Tyr Gly Phe  
 195 200 205  
 Ser Val Pro Met Ala Ser Val Leu Val Asp Val Ala Leu Ile Gly Ile  
 210 215 220  
 Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe Arg Leu Pro Ser Gln Asp  
 225 230 235 240  
 Ala Arg His Lys Ala Leu Asn Thr Cys Gly Ser His Ile Gly Val Ile  
 245 250 255  
 Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr Phe Leu Thr His Arg Phe  
 260 265 270  
 Gly Lys Asn Ile Pro His His Val His Ile Leu Leu Ala Asn Leu Tyr  
 275 280 285  
 Val Leu Val Pro Pro Met Leu Asn Pro Ile Ile Tyr Gly Ala Lys Thr  
 290 295 300  
 Lys Gln Ile Arg Asp Ser Met Thr Arg Met Leu Ser Val Val Trp Lys  
 305 310 315 320  
 Ser

<210> 57  
 <211> 326  
 <212> PRT  
 <213> Mus musculus

<400> 57  
 Met Lys Val Ala Ser Ser Phe His Asn Asp Thr Asn Pro Gln Asp Val  
 1 5 10 15  
 Trp Tyr Val Leu Ile Gly Ile Pro Gly Leu Glu Asp Leu His Ser Trp  
 20 25 30  
 Ile Ala Ile Pro Ile Cys Ser Met Tyr Ile Val Ala Val Ile Gly Asn  
 35 40 45

Val Leu Leu Ile Phe Leu Ile Val Thr Glu Arg Ser Leu His Glu Pro  
 50 55 60  
 Met Tyr Phe Phe Leu Ser Met Leu Ala Leu Ala Asp Leu Leu Leu Ser  
 65 70 75 80  
 Thr Ala Thr Ala Pro Lys Met Leu Ala Ile Phe Trp Phe His Ser Arg  
 85 90 95  
 Gly Ile Ser Phe Gly Ser Cys Val Ser Gln Met Phe Phe Ile His Phe  
 100 105 110  
 Ile Phe Val Ala Glu Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg  
 115 120 125  
 Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Ser  
 130 135 140  
 Ser Val Ile Gly Lys Ile Gly Thr Ala Ala Val Val Arg Ser Phe Leu  
 145 150 155 160  
 Ile Cys Phe Pro Phe Ile Phe Leu Val Tyr Arg Leu Leu Tyr Cys Gly  
 165 170 175  
 Lys His Ile Ile Pro His Ser Tyr Cys Glu His Met Gly Ile Ala Arg  
 180 185 190  
 Leu Ala Cys Asp Asn Ile Thr Val Asn Ile Ile Tyr Gly Leu Thr Met  
 195 200 205  
 Ala Leu Leu Ser Thr Gly Leu Asp Ile Leu Leu Ile Ile Ile Ser Tyr  
 210 215 220  
 Thr Met Ile Leu Arg Thr Val Phe Gln Ile Pro Ser Trp Ala Ala Arg  
 225 230 235 240  
 Tyr Lys Ala Leu Asn Thr Cys Gly Ser His Ile Cys Val Ile Leu Leu  
 245 250 255  
 Phe Tyr Thr Pro Ala Phe Phe Ser Phe Phe Ala His Arg Phe Gly Gly  
 260 265 270  
 Lys Thr Val Pro Arg His Ile His Ile Leu Val Ala Asn Leu Tyr Val  
 275 280 285  
 Val Val Pro Pro Met Leu Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys  
 290 295 300  
 Gln Ile Gln Asp Arg Val Val Phe Leu Phe Ser Ser Val Ser Thr Cys  
 305 310 315 320  
 Gln His Asp Ser Arg Cys  
 325

<210> 58

<211> 319

<212> PRT

<213> Mus musculus

<400> 58

Met Ala Thr Ser Asn Ser Ser Thr Ile Val Ser Ser Thr Phe Tyr Leu

|   |                     |                             |     |
|---|---------------------|-----------------------------|-----|
| 1   | 5                   | 10                          | 15  |
| Thr Gly Ile Pro   | Gly Tyr Glu Glu Phe | His His Trp Ile Ser Ile Pro |     |
| 20  | 25                  | 30                          |     |
| Phe Cys Phe Leu Tyr Leu Val Gly Ile Thr Gly Asn Cys Met Ile Leu |                     |                             |     |
| 35  | 40                  | 45                          |     |
| His Ile Val Arg Thr Asp Pro Arg Leu His Glu Pro Met Tyr Tyr Phe |                     |                             |     |
| 50  | 55                  | 60                          |     |
| Leu Ala Met Leu Ser Leu Thr Asp Met Ala Met Ser Leu Pro Thr Met |                     |                             |     |
| 65  | 70                  | 75                          | 80  |
| Met Ser Leu Phe Arg Val Leu Trp Ser Ile Ser Arg Glu Ile Gln Phe |                     |                             |     |
| 85  | 90                  | 95                          |     |
| Asn Ile Cys Val Val Gln Met Phe Leu Ile His Thr Phe Ser Phe Thr |                     |                             |     |
| 100   | 105                 | 110                         |     |
| Glu Ser Ser Val Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile |                     |                             |     |
| 115   | 120                 | 125                         |     |
| Cys His Pro Leu Arg Tyr Ala Thr Ile Leu Thr Pro Lys Leu Ile Ala |                     |                             |     |
| 130   | 135                 | 140                         |     |
| Lys Ile Gly Thr Ala Ala Leu Leu Arg Ser Ser Ile Leu Ile Ile Pro |                     |                             |     |
| 145   | 150                 | 155                         | 160 |
| Leu Ile Ala Arg Leu Ala Phe Phe Pro Phe Cys Gly Ser His Val Leu |                     |                             |     |
| 165   | 170                 | 175                         |     |
| Ser His Ser Tyr Cys Leu His Gln Asp Met Ile Arg Leu Ala Cys Ala |                     |                             |     |
| 180   | 185                 | 190                         |     |
| Asp Ile Arg Phe Asn Val Ile Tyr Gly Leu Val Leu Ile Thr Leu Leu |                     |                             |     |
| 195   | 200                 | 205                         |     |
| Trp Gly Met Asp Ser Leu Gly Ile Phe Val Ser Tyr Val Leu Ile Leu |                     |                             |     |
| 210   | 215                 | 220                         |     |
| His Ser Val Leu Lys Ile Ala Ser Arg Glu Gly Arg Leu Lys Ala Leu |                     |                             |     |
| 225   | 230                 | 235                         | 240 |
| Asn Thr Cys Ala Ser His Ile Cys Ala Val Leu Ile Leu Tyr Val Pro |                     |                             |     |
| 245   | 250                 | 255                         |     |
| Met Ile Gly Leu Ser Ile Val His Arg Phe Ala Lys His Ser Ser Pro |                     |                             |     |
| 260   | 265                 | 270                         |     |
| Leu Ile His Ile Phe Met Ala His Ile Tyr Leu Leu Val Pro Pro Val |                     |                             |     |
| 275   | 280                 | 285                         |     |
| Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg Glu Gly |                     |                             |     |
| 290   | 295                 | 300                         |     |
| Ile Leu His Leu Leu Cys Ser Pro Lys Ile Ser Ser Ile Thr Met     |                     |                             |     |
| 305   | 310                 | 315                         |     |

<210> 59  
 <211> 317  
 <212> PRT

<213> Mus musculus

<400> 59

Met Lys Val Ser Ile Pro Pro Arg Ala Asn Phe Ser Tyr Ala Ile Phe  
1 5 10 15  
Leu Leu Thr Gly Phe Pro Gly Leu Glu Trp Ala His His Trp Ile Ser  
20 25 30  
Leu Pro Ile Phe Met Gly Tyr Phe Val Ala Ile Met Gly Asn Ala Thr  
35 40 45  
Ile Leu His Leu Val Arg Thr Asp Pro Ser Leu His Gln Pro Met Tyr  
50 55 60  
Tyr Phe Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Cys Met Ser  
65 70 75 80  
Thr Leu Pro Ser Val Leu Gly Val Leu Trp Phe Asp Ala Arg Met Val  
85 90 95  
Gly Leu Val Pro Cys Val Leu Gln Gln His Phe Leu His Ser Phe Ser  
100 105 110  
Phe Met Glu Ser Ala Val Leu Phe Ala Met Ala Leu Asp Arg Leu Ile  
115 120 125  
Ala Ile Arg Phe Pro Leu Arg Tyr Ala Ser Val Leu Thr Gly Pro Arg  
130 135 140  
Val Ala Leu Ile Gly Thr Val Leu Gly Met Arg Ser Ala Ala Ile Thr  
145 150 155 160  
Ala Ala Pro Ser Leu His Leu Leu Thr Phe Asp Tyr Cys His Pro Gly  
165 170 175  
Ala Leu Ser His Ala Tyr Cys Leu His Gln Asp Met Ile Arg Leu Ala  
180 185 190  
Cys Ser Asp Thr Arg Phe Asn Arg Leu Tyr Gly Leu Cys Ile Ile Met  
195 200 205  
Leu Ala Met Gly Ser Asp Val Leu Phe Ile Leu Leu Ser Tyr Ala Val  
210 215 220  
Ile Leu Arg Thr Val Leu Ala Ile Ala Ser Ala Gly Glu Arg Leu Lys  
225 230 235 240  
Ala Leu Asn Thr Cys Val Ser His Ile Leu Ala Val Leu Cys Phe Tyr  
245 250 255  
Val Pro Val Leu Gly Leu Ser Ile Val His Arg Phe Gly Gln His Thr  
260 265 270  
Ser Pro Leu Val His Ile Leu Met Gly Thr Val Ser Val Leu Phe Pro  
275 280 285  
Pro Val Met Asn Pro Val Ile Tyr Ser Ile Lys Thr Gln Gln Ile Arg  
290 295 300  
Arg Ala Ile Val Lys Val Ile Ser Leu Gly Lys Ile Gln  
305 310 315

<210> 60  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 60

```

Met Leu Gly Leu Asn Gly Thr Pro Phe Gln Pro Ala Thr Leu Gln Leu
  1                      5                      10                      15

Thr Gly Ile Pro Gly Ile Gln Thr Gly Leu Thr Trp Val Ala Leu Ile
                20                      25                      30

Phe Cys Ile Leu Tyr Met Ile Ser Ile Val Gly Asn Leu Ser Ile Leu
                35                      40                      45

Thr Leu Val Phe Trp Glu Pro Ala Leu His Gln Pro Met Tyr Tyr Phe
                50                      55                      60

Leu Ser Met Leu Ala Leu Asn Asp Leu Gly Val Ser Phe Ser Thr Leu
  65                      70                      75                      80

Pro Thr Val Ile Ser Thr Phe Cys Phe Asn Tyr Asn His Val Ala Phe
                85                      90                      95

Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Ser Phe Met
                100                     105                     110

Glu Ser Gly Ile Leu Leu Ala Met Ser Leu Asp Arg Phe Val Ala Ile
                115                     120                     125

Cys Tyr Pro Leu Arg Tyr Val Thr Val Leu Thr His Asn Arg Ile Leu
                130                     135                     140

Ala Met Gly Leu Gly Ile Leu Thr Lys Ser Phe Thr Thr Leu Phe Pro
  145                     150                     155                     160

Phe Pro Phe Val Val Lys Arg Leu Pro Phe Cys Lys Gly Asn Val Leu
                165                     170                     175

His His Ser Tyr Cys Leu His Pro Asp Leu Met Lys Val Ala Cys Gly
                180                     185                     190

Asp Ile His Val Asn Asn Ile Tyr Gly Leu Leu Val Ile Ile Phe Thr
                195                     200                     205

Tyr Gly Met Asp Ser Thr Phe Ile Leu Leu Ser Tyr Ala Leu Ile Leu
                210                     215                     220

Arg Ala Met Leu Val Ile Ile Ser Gln Glu Gln Arg Leu Lys Ala Leu
  225                     230                     235                     240

Asn Thr Cys Met Ser His Ile Cys Ala Val Leu Ala Phe Tyr Val Pro
                245                     250                     255

Ile Ile Ala Val Ser Met Ile His Arg Phe Trp Lys Ser Ala Pro Pro
                260                     265                     270

Val Val His Val Met Met Ser Asn Val Tyr Leu Phe Val Pro Pro Met
                275                     280                     285

Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Glu Ile Arg Lys Gly
  290                     295                     300

```

Ile Leu Lys Phe Phe His Lys Ser Gln Ala  
305 310

<210> 61  
<211> 312  
<212> PRT  
<213> Homo sapiens

<400> 61  
Met Gly Leu Phe Asn Val Thr His Pro Ala Phe Phe Leu Leu Thr Gly  
1 5 10 15

Ile Pro Gly Leu Glu Ser Ser His Ser Trp Leu Ser Gly Pro Leu Cys  
20 25 30

Val Met Tyr Ala Val Ala Leu Gly Gly Asn Thr Val Ile Leu Gln Ala  
35 40 45

Val Arg Val Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ser  
50 55 60

Met Leu Ser Phe Ser Asp Val Ala Ile Ser Met Ala Thr Leu Pro Thr  
65 70 75 80

Val Leu Arg Thr Phe Cys Leu Asn Ala Arg Asn Ile Thr Phe Asp Ala  
85 90 95

Cys Leu Ile Gln Met Phe Leu Ile His Phe Phe Ser Met Met Glu Ser  
100 105 110

Gly Ile Leu Leu Ala Met Ser Phe Asp Arg Tyr Val Ala Ile Cys Asp  
115 120 125

Pro Leu Arg Tyr Ala Thr Val Leu Thr Thr Glu Val Ile Ala Ala Met  
130 135 140

Gly Leu Gly Ala Ala Ala Arg Ser Phe Ile Thr Leu Phe Pro Leu Pro  
145 150 155 160

Phe Leu Ile Lys Arg Leu Pro Ile Cys Arg Ser Asn Val Leu Ser His  
165 170 175

Ser Tyr Cys Leu His Pro Asp Met Met Arg Leu Ala Cys Ala Asp Ile  
180 185 190

Ser Ile Asn Ser Ile Tyr Gly Leu Phe Val Leu Val Ser Thr Phe Gly  
195 200 205

Met Asp Leu Phe Phe Ile Phe Leu Ser Tyr Val Leu Ile Leu Arg Ser  
210 215 220

Val Met Ala Thr Ala Ser Arg Glu Glu Arg Leu Lys Ala Leu Asn Thr  
225 230 235 240

Cys Val Ser His Ile Leu Ala Val Leu Ala Phe Tyr Val Pro Met Ile  
245 250 255

Gly Val Ser Thr Val His Arg Phe Gly Lys His Val Pro Cys Tyr Ile  
260 265 270

His Val Leu Met Ser Asn Val Tyr Leu Phe Val Pro Pro Val Leu Asn

275

280

285

Pro Leu Ile Tyr Ser Ala Lys Thr Lys Glu Ile Arg Arg Ala Ile Phe  
 290 295 300

Arg Met Phe His His Ile Lys Ile  
 305 310

&lt;210&gt; 62

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

Met Ser Ser Ser Ser Ser His Pro Phe Leu Leu Thr Gly Phe Pro  
 1 5 10 15

Gly Leu Glu Glu Ala His His Trp Ile Ser Val Phe Phe Leu Phe Met  
 20 25 30

Tyr Ile Ser Ile Leu Phe Gly Asn Gly Thr Leu Leu Leu Ile Lys  
 35 40 45

Glu Asp His Asn Leu His Glu Pro Met Tyr Phe Phe Leu Ala Met Leu  
 50 55 60

Ala Ala Thr Asp Leu Gly Leu Ala Leu Thr Thr Met Pro Thr Val Leu  
 65 70 75 80

Gly Val Leu Trp Leu Asp His Arg Glu Ile Gly Ser Ala Ala Cys Phe  
 85 90 95

Ser Gln Ala Tyr Phe Ile His Ser Leu Ser Phe Leu Glu Ser Gly Ile  
 100 105 110

Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Asn Pro Leu  
 115 120 125

Arg Tyr Thr Ser Val Leu Thr Asn Thr Arg Val Val Lys Ile Gly Leu  
 130 135 140

Gly Val Leu Met Arg Gly Phe Val Ser Val Val Pro Pro Ile Arg Pro  
 145 150 155 160

Leu Tyr Phe Phe Leu Tyr Cys His Ser His Val Leu Ser His Ala Phe  
 165 170 175

Cys Leu His Gln Asp Val Ile Lys Leu Ala Cys Ala Asp Thr Thr Phe  
 180 185 190

Asn Arg Leu Tyr Pro Ala Val Leu Val Val Phe Ile Phe Val Leu Asp  
 195 200 205

Tyr Leu Ile Ile Phe Ile Ser Tyr Val Leu Ile Leu Lys Thr Val Leu  
 210 215 220

Ser Ile Ala Ser Arg Glu Glu Arg Ala Lys Ala Leu Ile Thr Cys Val  
 225 230 235 240

Ser His Ile Cys Cys Val Leu Val Phe Tyr Val Thr Val Ile Gly Leu  
 245 250 255

Ser Leu Ile His Arg Phe Gly Lys Gln Val Pro His Ile Val His Leu  
 260 265 270

Ile Met Ser Tyr Ala Tyr Phe Leu Phe Pro Pro Leu Met Asn Pro Ile  
 275 280 285

Thr Tyr Ser Val Lys Thr Lys Gln Ile Gln Asn Ala Ile Leu His Leu  
 290 295 300

Phe Thr Thr His Arg Ile Gly Thr  
 305 310

<210> 63  
 <211> 318  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> VARIANT  
 <222> (286)  
 <223> Wherein Xaa is any amino acid.

<400> 63  
 Met Ser Pro Gly Asn Ser Ser Trp Ile His Pro Ser Ser Phe Leu Leu  
 1 5 10 15

Leu Gly Ile Pro Gly Leu Glu Glu Leu Gln Phe Trp Leu Gly Leu Pro  
 20 25 30

Phe Gly Thr Val Tyr Leu Ile Ala Val Leu Gly Asn Val Ile Ile Leu  
 35 40 45

Phe Val Ile Tyr Leu Glu His Ser Leu His Gln Pro Met Phe Tyr Leu  
 50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Ser Thr Ala Thr Val  
 65 70 75 80

Pro Arg Ala Leu Gly Ile Phe Trp Phe Gly Phe His Lys Ile Ala Phe  
 85 90 95

Arg Asp Cys Val Ala Gln Met Phe Phe Ile His Leu Phe Thr Gly Ile  
 100 105 110

Glu Thr Phe Met Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile  
 115 120 125

Cys Asn Pro Leu Arg Tyr Asn Thr Ile Leu Thr Asn Arg Thr Ile Cys  
 130 135 140

Ile Ile Val Gly Val Gly Leu Phe Lys Asn Phe Ile Leu Val Phe Pro  
 145 150 155 160

Leu Ile Phe Leu Ile Leu Arg Leu Ser Phe Cys Gly His Asn Ile Ile  
 165 170 175

Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Val  
 180 185 190

Ser Ile Lys Val Asn Val Leu Phe Gly Leu Ile Leu Ile Ser Met Ile  
 195 200 205



Leu Leu Asp Val Val Leu Ser Ala Leu Ser Tyr Ala Lys Ile Leu His  
 210 215 220  
 Ala Val Phe Lys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn  
 225 230 235 240  
 Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Phe Thr Pro Ala  
 245 250 255  
 Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Arg Tyr  
 260 265 270  
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Ile Ile Pro Xaa Ala Leu  
 275 280 285  
 Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Asp Arg Ala  
 290 295 300  
 Val Thr Ile Leu Cys Asn Glu Val Gly Gln Leu Ala Asp Asp  
 305 310 315  
 <210> 64  
 <211> 320  
 <212> PRT  
 <213> Rattus norvegicus  
 <400> 64  
 Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Met Leu Ile Gly Ile  
 1 5 10 15  
 Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser  
 20 25 30  
 Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val  
 35 40 45  
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
 50 55 60  
 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
 65 70 75 80  
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys  
 85 90 95  
 Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr  
 100 105 110  
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
 115 120 125  
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly  
 130 135 140  
 Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Pro Leu Pro Leu  
 145 150 155 160  
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser  
 165 170 175  
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu  
 180 185 190

Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val  
195 200 205

Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val  
210 215 220

Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys  
225 230 235 240

Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly  
245 250 255

Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His  
260 265 270

Val Leu Met Gly Asp Val Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro  
275 280 285

Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala  
290 295 300

Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr  
305 310 315 320

<210> 65

<211> 320

<212> PRT

<213> Homo sapiens

<400> 65

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile  
1 5 10 15

Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser  
20 25 30

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val  
35 40 45

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
50 55 60

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
65 70 75 80

Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys  
85 90 95

Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr  
100 105 110

Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
115 120 125

Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly  
130 135 140

Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Pro Leu Pro Leu  
58



Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Ile Pro Leu Arg His Ala Thr Ile Phe Ser Gln Gln Phe Leu Thr  
 130 135 140  
 His Ile Gly Leu Gly Val Thr Leu Arg Ala Ala Ile Leu Ile Ile Pro  
 145 150 155 160  
 Ser Leu Gly Leu Ile Lys Cys Cys Leu Lys His Tyr Arg Thr Thr Val  
 165 170 175  
 Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Thr  
 180 185 190  
 Glu Asp Ile Arg Val Asn Lys Ile Tyr Gly Leu Phe Val Ala Phe Ala  
 195 200 205  
 Ile Leu Gly Phe Asp Ile Ile Phe Ile Thr Leu Ser Tyr Val Gln Ile  
 210 215 220  
 Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala  
 225 230 235 240  
 Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu  
 245 250 255  
 Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ser His Ile Pro  
 260 265 270  
 Pro Tyr Ile His Ile Leu Leu Ser Asn Leu Tyr Leu Leu Val Pro Pro  
 275 280 285  
 Phe Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp  
 290 295 300  
 His Ile Val Lys Val Phe Phe Phe Lys Lys Val Thr  
 305 310 315

<210> 67  
 <211> 316  
 <212> PRT  
 <213> Mus musculus

<400> 67  
 Met Pro His Leu Asn Ser Thr Ile Phe Arg Pro Ser Val Leu Thr Leu  
 1 5 10 15  
 Thr Gly Ile Pro Gly Leu Glu Ser Val Gln Phe Trp Ile Gly Ile Pro  
 20 25 30  
 Phe Cys Ile Met Tyr Ile Ile Ala Leu Leu Gly Asn Ser Leu Leu Leu  
 35 40 45  
 Val Val Ile Lys Val Glu Arg Ser Leu His Glu Pro Met Tyr Leu Phe  
 50 55 60  
 Leu Ala Met Leu Gly Ala Thr Asp Ile Ser Leu Ser Thr Ser Ile Leu  
 65 70 75 80  
 Pro Lys Met Leu Gly Ile Phe Trp Phe His Leu Ser Thr Ile Tyr Phe  
 85 90 95

Asp Ala Cys Leu Leu Gln Met Trp Leu Ile His Thr Phe Gln Gly Ile  
 100 105 110  
 Glu Ser Gly Ile Leu Phe Ala Met Ala Met Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Asp Pro Leu Arg His Ala Ser Ile Phe Thr Gln Arg Leu Leu Thr  
 130 135 140  
 Gln Ile Gly Val Gly Val Thr Leu Arg Ala Ala Leu Phe Val Ala Pro  
 145 150 155 160  
 Cys Leu Phe Leu Ile Lys Cys Arg Leu Lys Phe Tyr Trp Thr Thr Val  
 165 170 175  
 Val Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala  
 180 185 190  
 Glu Asp Val His Val Asn Lys Ile Tyr Gly Leu Phe Val Ala Phe Ser  
 195 200 205  
 Ile Leu Gly Leu Asp Ile Ile Phe Ile Thr Leu Ser Tyr Ile Arg Ile  
 210 215 220  
 Phe Ile Thr Val Phe Lys Leu Pro Gln Lys Glu Ala Arg Leu Lys Ala  
 225 230 235 240  
 Phe Asn Thr Cys Val Ala His Ile Cys Val Phe Leu Glu Phe Tyr Leu  
 245 250 255  
 Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Tyr His Val Pro  
 260 265 270  
 Ser Tyr Ile His Ile Leu Leu Ser Asn Leu Tyr Leu Leu Val Pro Pro  
 275 280 285  
 Leu Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp  
 290 295 300  
 Gln Val Ser Lys Ile Leu Tyr Cys Asn Tyr Ser Tyr  
 305 310 315

<210> 68

<211> 315

<212> PRT

<213> Mus musculus

<400> 68

Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro Ser Val Leu Thr Leu  
 1 5 10 15  
 Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro  
 20 25 30  
 Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly Asn Ser Leu Ile Leu  
 35 40 45  
 Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile Pro Met Tyr Ile Phe  
 50 55 60  
 Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu Ser Thr Cys Ile Leu  
 61



Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile Pro Met Tyr Ile Phe  
 50 55 60  
 Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu Ser Thr Cys Ile Leu  
 65 70 75 80  
 Pro Lys Met Leu Gly Ile Phe Trp Phe His Met Pro Gln Ile Ser Phe  
 85 90 95  
 Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His Ser Phe Gln Ala Thr  
 100 105 110  
 Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile  
 115 120 125  
 Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser Pro Gln Leu Thr Thr  
 130 135 140  
 Cys Leu Gly Ala Gly Ala Leu Leu Arg Ser Leu Ile Thr Thr Phe Pro  
 145 150 155 160  
 Leu Ile Leu Leu Ile Lys Phe Cys Leu Lys Tyr Phe Arg Thr Thr Ile  
 165 170 175  
 Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala  
 180 185 190  
 Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu Leu Val Ala Phe Ala  
 195 200 205  
 Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe Ser Tyr Val Arg Ile  
 210 215 220  
 Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala  
 225 230 235 240  
 Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu  
 245 250 255  
 Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ala His Ile Pro  
 260 265 270  
 Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr Leu Leu Val Pro Pro  
 275 280 285  
 Phe Leu Asn Pro Ile Val Tyr Gly Ile Lys Thr Lys Gln Ile Arg Asp  
 290 295 300  
 Gln Val Leu Lys Met Phe Phe Ser Lys Lys Pro Leu  
 305 310 315

<210> 70  
 <211> 319  
 <212> PRT  
 <213> Gallus gallus

<400> 70  
 Met Tyr Pro Arg Asn Ser Ser Gln Ala Gln Pro Phe Leu Leu Ala Gly  
 1 5 10 15  
 Leu Pro Gly Met Ala Gln Phe His His Trp Val Phe Leu Pro Phe Gly  
 20 25 30

Leu Met Tyr Leu Val Ala Val Leu Gly Asn Gly Thr Ile Leu Leu Val  
 35 40 45  
 Val Arg Val His Arg Gln Leu His Gln Pro Met Tyr Tyr Phe Leu Leu  
 50 55 60  
 Met Leu Ala Thr Thr Asp Leu Gly Leu Thr Leu Ser Thr Leu Pro Thr  
 65 70 75 80  
 Val Leu Arg Val Phe Trp Leu Gly Ala Met Glu Ile Ser Phe Pro Ala  
 85 90 95  
 Cys Leu Ile Gln Met Phe Cys Ile His Val Phe Ser Phe Met Glu Ser  
 100 105 110  
 Ser Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Cys  
 115 120 125  
 Pro Leu Arg Tyr Ser Ser Ile Leu Thr Gly Ala Arg Val Ala Gln Ile  
 130 135 140  
 Gly Leu Gly Ile Ile Cys Arg Cys Thr Leu Ser Leu Leu Pro Leu Ile  
 145 150 155 160  
 Cys Leu Leu Thr Trp Leu Pro Phe Cys Arg Ser His Val Leu Ser His  
 165 170 175  
 Pro Tyr Cys Leu His Gln Asp Ile Ile Arg Leu Ala Cys Thr Asp Ala  
 180 185 190  
 Thr Leu Asn Ser Leu Tyr Gly Leu Ile Leu Val Leu Val Ala Ile Leu  
 195 200 205  
 Asp Phe Val Leu Ile Ala Leu Ser Tyr Ile Met Ile Phe Arg Thr Val  
 210 215 220  
 Leu Gly Ile Thr Ser Lys Glu Glu Gln Thr Lys Ala Leu Asn Thr Cys  
 225 230 235 240  
 Val Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu Ala Gly  
 245 250 255  
 Leu Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pro Ile Ser His  
 260 265 270  
 Ala Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu Asn Pro  
 275 280 285  
 Val Leu Tyr Ser Met Lys Ser Lys Ala Ile Cys Lys Gly Leu Leu Arg  
 290 295 300  
 Leu Leu Cys Gln Arg Ala Ala Trp Pro Gly His Ala Gln Asn Cys  
 305 310 315

<210> 71

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00001



7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 71

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
1 5 10 15

Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
20 25 30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
35 40 45

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe  
50 55 60

Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile  
65 70 75 80

Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg  
85 90 95

Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
100 105 110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
115 120 125

Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser  
130 135 140

Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu  
145 150 155 160

Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
165 170 175

Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
180 185 190

Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Phe Val  
195 200 205

Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys  
210 215 220

Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
225 230 235 240

Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
245 250

<210> 72

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00001

7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 72

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg

| 1   | 5   | 10  | 15  |
|---|-----|-----|-----|
| Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu | 20  | 25  | 30  |
| Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly | 35  | 40  | 45  |
| Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe | 50  | 55  | 60  |
| Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Thr Ala Ile Ser Ile     | 65  | 70  | 80  |
| Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg | 85  | 90  | 95  |
| Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala | 100 | 105 | 110 |
| Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val | 115 | 120 | 125 |
| Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser | 130 | 135 | 140 |
| Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu | 145 | 150 | 155 |
| Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu | 165 | 170 | 175 |
| Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser | 180 | 185 | 190 |
| Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Phe Val     | 195 | 200 | 205 |
| Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys | 210 | 215 | 220 |
| Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu | 225 | 230 | 235 |
| Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr         | 245 | 250 |     |

<210> 73

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00001

7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 73

|   |   |   |    |    |
|---|---|---|----|----|
| Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg | 1 | 5 | 10 | 15 |
|---|---|---|----|----|

|   |    |    |    |
|---|----|----|----|
| Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu | 20 | 25 | 30 |
|---|----|----|----|

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
           35                          40                          45  
 Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe  
           50                          55                          60  
 Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile  
           65                          70                          75                          80  
 Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg  
                           85                          90                          95  
 Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
                           100                          105                          110  
 Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
                           115                          120                          125  
 Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser  
           130                          135                          140  
 Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu  
           145                          150                          155                          160  
 Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
                           165                          170                          175  
 Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
                           180                          185                          190  
 Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val  
                           195                          200                          205  
 Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys  
           210                          215                          220  
 Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
           225                          230                          235                          240  
 Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
                           245                          250

<210> 74

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00001

7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 74

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
           1                          5                          10                          15

Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
           20                          25                          30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
           35                          40                          45

```

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe
 50                      55                      60

Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile
 65                      70                      75                      80

Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg
                      85                      90                      95

Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala
          100                      105                      110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val
          115                      120                      125

Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser
          130                      135                      140

Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu
          145                      150                      155                      160

Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu
          165                      170                      175

Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser
          180                      185                      190

Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val
          195                      200                      205

Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys
          210                      215                      220

Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu
          225                      230                      235                      240

Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr
          245                      250

```

<210> 75

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00001  
7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 75

```

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
 1                      5                      10                      15

Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu
          20                      25                      30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
          35                      40                      45

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe
          50                      55                      60

Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile
          65

```



Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
100 105 110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
115 120 125

Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser  
130 135 140

Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu  
145 150 155 160

Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
165 170 175

Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
180 185 190

Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val  
195 200 205

Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys  
210 215 220

Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
225 230 235 240

Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
245 250

<210> 77  
<211> 254  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:pfam00001  
7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 77  
Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
1 5 10 15  
Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
20 25 30  
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
35 40 45  
Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe  
50 55 60  
Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile  
65 70 75 80  
Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg  
85 90 95  
Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
100 105 110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
 115 120 125  
 Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser  
 130 135 140  
 Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu  
 145 150 155 160  
 Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
 165 170 175  
 Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
 180 185 190  
 Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Phe Val  
 195 200 205  
 Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys  
 210 215 220  
 Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
 225 230 235 240  
 Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
 245 250  
  
 <210> 78  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:pfam00001  
 7tm\_1, 7 transmembrane receptor (rhodopsin family)  
  
 <400> 78  
 Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
 1 5 10 15  
 Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
 20 25 30  
 Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
 35 40 45  
 Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe  
 50 55 60  
 Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile  
 65 70 75 80  
 Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg  
 85 90 95  
 Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
 100 105 110  
 Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
 115 120 125  
 Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser  
 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250

130 135 140

Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu  
145 150 155 160

Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
165 170 175

Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
180 185 190

Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Phe Val  
195 200 205

Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys  
210 215 220

Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
225 230 235 240

Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
245 250

<210> 79  
<211> 254  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:pfam00001  
7tm\_1, 7 transmembrane receptor (rhodopsin family)

<400> 79  
Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg  
1 5 10 15

Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
20 25 30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
35 40 45

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe  
50 55 60

Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile  
65 70 75 80

Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg  
85 90 95

Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
100 105 110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
115 120 125

Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser  
130 135 140

Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu  
145 150 155 160



Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
165 170  
Arg Lys Ser Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
180 185 190  
Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Val Phe Val  
195 200 205  
Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys  
210 215 220  
Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
225 230 235 240  
Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
245 250

<210> 80  
<211> 981  
<212> DNA  
<213> Homo sapiens  
<400> 80  
tgatgctggg tccagcttat aaccacacaa tggaaacccc tgcctccttc ctcttctggg 60  
gtatcccagg actgcaatct tcacatcttt ggctggctat ctcaactgagt gccatgtaca 120  
tcatagccct gtttaggaaac accctcatcg tgactgcaat ctggatggat tccactcggc 180  
atgagcccat gtattgcttt ctgtgtgttc tggctgctgt ggacattgtt atggcctctc 240  
ccgttggtacc caagatgggt agcatcttct gctcgggaga cagctccatc agctttagtg 300  
cttggtttcac tcagatgttt tttgtccact tagccacagc tgtggagacg gggtgtctgc 360  
tgaccatggc ttttgaccgc tatgtagcca tctgcaagcc tctacactac aagagaattc 420  
tcacgcccga agtggatgct ggaatgagta tggccgtcac catcagagct gtcacattca 480  
tgactccact gagttggatg atgaatcacc tacctttctg ttgctccaat gtggttgctc 540  
actcctactg taagcacata gctttggcca ggtagcatg tgctgacccc gtgcccagca 600  
gtctctacag tctgattggg tcctctctta tgggtgggctc tgatgtggcc ttcatgtctg 660  
ctctctatat cttaattctc agggcagtat ttgatctctc ctcaaagact gctcagttga 720  
aagcattaag cacatgtggc tcccatgtgg gggttatggc ttgtactat ctacctggga 780  
tggcatccat ctatgccgcc tgggtggggc aggatatagt gcccttgac acccaagtgc 840  
tgctagctga cctgtacgtg atcatccag ccactttaa tcccatcacc tatggcatga 900  
ggaccaaaca attgctggag ggaatatgga gttatctgat gcactgtcct ctttgaccac 960  
tccaaactgg gttcatgaac a 981

<210> 81  
<211> 317  
<212> PRT  
<213> Homo sapiens  
<400> 81  
Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe  
1 5 10 15  
Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala  
20 25 30  
Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Leu  
35 40 45  
Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr  
50 55 60

Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser  
 65 70 75 80  
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile  
 85 90 95  
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr  
 100 105 110  
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val  
 115 120 125  
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val  
 130 135 140  
 Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met  
 145 150 155 160  
 Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn  
 165 170 175  
 Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala  
 180 185 190  
 Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser  
 195 200 205  
 Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu  
 210 215 220  
 Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys  
 225 230 235 240  
 Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr  
 245 250 255  
 Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile  
 260 265 270  
 Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile  
 275 280 285  
 Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu  
 290 295 300  
 Leu Glu Gly Ile Trp Ser Tyr Leu Met His Cys Pro Leu  
 305 310 315

<210> 82  
 <211> 982  
 <212> DNA  
 <213> Homo sapiens

<400> 82  
 ttgatgctgg gtccagctta caaccacaca atggaaaccc ctgcctcctt cctccttggt 60  
 ggatccccag gactgcaatc ttcacatctt tggctgggcta tctcactgag tgccatgtac 120  
 atcatagccc tgttaggaaa caccctcatc gtgactgcaa tctggatgga ttccactcgg 180  
 catgagccca tgtattgctt tctgtgtgtt ctggctgctg tggacattgt tatggcctcc 240  
 tctggtggtac ccaagatggt gagcatcttc tgctcgggag acagctccat cagctttagt 300  
 gcttgtttca ctccagatggt ttttgtccac ttagccacac ctgtggagac ggggctgctg 360  
 ctgaccatgg cttttgaccg ctatgtagcc atctgcaagc ctctacacta caagagaatt 420  
 ctccagcctc aagtgatgct gggaatgagt atggccgtca ccatcagagc tgtcacattc 480

```

atgactccac  tgagttggat  gatgaatcat  ctacctttct  gtggctccaa  tgtggtgtgc  540
cactectact  gtaagcacat  agctttggcc  aggttagcat  gtgctgacc  cgtgcccagc  600
agcctctaca  gtctgattgg  ttctctctct  atggtgggct  ctgagtgtgc  ctctattgtg  660
gcctectata  tcttaattct  cagggcagta  ttgatctct  cctcaaagac  tgctcagttg  720
aaagcattaa  gcacatgtgg  ctcccatgtg  ggggttatgg  ctttgtacta  tctacctggg  780
atggcatcca  tctatgcggc  ctggttgggg  caggatatag  tgccttgca  cacccaagtg  840
ctgctagctg  acctgtacct  gatcatccca  gccactttaa  atcccatcat  ctatggcatg  900
aggaccaaac  aattgctgga  gggaatatgg  agttatctga  tgcacttctc  ctttgaccac  960
tccaacctgg  gttcatgaac  aa

```

```

<210> 83
<211> 324
<212> PRT
<213> Homo sapiens

```

```

<400> 83
Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe
  1           5           10           15
Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
      20           25           30
Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Leu
      35           40           45
Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
      50           55           60
Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
      65           70           75           80
Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
      85           90           95
Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
      100          105          110
Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
      115          120          125
Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
      130          135          140
Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met
      145          150          155          160
Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn
      165          170          175
Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala
      180          185          190
Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
      195          200          205
Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
      210          215          220
Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys
      225          230          235          240
Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr

```

